

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:47:36 ; Search time 5329.58 seconds
(without alignments)
10646.432 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171
Sequence: 1 atgaagtcgctcctacacg.....acatggaatccagctctgta 1171

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	83.6	1488	6	AR075987 Sequence
2	979	83.6	1488	6	AR371655 Sequence
3	979	83.6	2970	9	BC040968 Homo sapi
4	847	72.3	1216	6	AR270911 Sequence
5	847	72.3	1216	9	HSU31332 Human DP pr
6	847	72.3	156808	2	AC012407 Homo sapi
7	847	72.3	187947	9	AC012407 Homo sapi
8	847	72.3	197817	9	AL356833 Human chr
9	556	47.5	1315	10	CNS05TCS
10	554.4	47.3	1074	10	RU92289
11	554.4	47.3	1240	6	AF120101 Rattus no
12	552.8	47.2	1071	6	E10040 Base sequen
13	544.8	46.5	895	10	E10039 Base sequen
14	541.6	46.3	67632	2	D29764 Mus musculi
15	541.6	46.3	110000	2	AC112324_0
16	541.6	46.3	110000	2	AC112324_1
17	541.6	46.3	110000	2	AC115635_2
18	541.6	46.3	299134	2	AC128783 Rattus no
19	541.6	46.3	349877	2	AC115218 Rattus no

C	20	538.4	46.0	57027	2	AC112324_3	Continuation (4 of
C	21	538.4	46.0	110000	2	AC095991_0	AC095991 Rattus no
C	22	538.4	46.0	110000	2	AC099237_3	Continuation (4 of
C	23	538.4	46.0	110000	2	AC099237_4	Continuation (4 of
C	24	538.4	46.0	110000	2	AC115635_1	Continuation (2 of
C	25	538.4	46.0	254094	2	AC120220	AC120220 Rattus no
C	26	538.4	46.0	349877	2	AC115218	AC115218 Rattus no
C	27	360	30.7	205345	2	AC128247	AC128247 Rattus no
C	28	360	30.7	232703	2	AC098748	AC098748 Rattus no
C	29	335	28.6	495	6	AX549001	AX549001 Sequence
C	30	335	28.6	495	9	HSU31039	U31039 Human DP pr
C	31	228.8	19.5	2935	4	AY166779	AY166779 Oryctolag
C	32	217.8	18.6	1428	4	BT293039	293039 B.taurus pr
C	33	211	18.0	1077	9	AY275471	AY275471 Homo sapi
C	34	211	18.0	1077	9	HSER2PR	X81668 H.sapiens m
C	35	211	18.0	2286	6	I88011	I88011 Sequence 3
C	36	211	18.0	2286	6	AR372105	AR372105 Sequence
C	37	211	18.0	2373	6	CQ720365	AF0720365 Sequence
C	38	210.8	18.0	2550	4	AF075602	AF075602 Canis fam
C	39	210.2	18.0	161100	2	CO867605	AC025659 Homo sapi
C	40	209.4	17.9	2372	6	AR270878	CO867605 Sequence
C	41	209.4	17.9	2372	6	AX549005	AR270878 Sequence
C	42	209.4	17.9	2372	6	HSU19487	AX549005 Sequence
C	43	209.4	17.9	2372	9	HSU19487	U19487 Human prot
C	44	209.4	17.9	6446	6	AR208580	AR208580 Sequence
C	45	208.6	17.8	3875	9	HSPTGER2G1	AF134201 Homo sapi

ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	4 from patent US 5958723.	DNA	linear	PAT 30-AUG-2000
AR075987	Sequence	AR075987	GI:10002733			
AR075987	Accession	AR075987	GI:10002733			
AR075987	Version	AR075987.1	GI:10002733			
AR075987	KeyWords	Unknown.				
AR075987	Source	Unknown.				
AR075987	Organism	Unclassified.				
AR075987	Reference	1 (bases 1 to 1488)				
AR075987	Authors	Abrahamovitz, M., Bole, Y., Metters, K., Sawyer, N. and Slipeck, D.M.				
AR075987	Title	DNA encoding prostaglandin receptor DP				
AR075987	Journal	Patent: US 5958723-A 4 28-SEP-1999;				
AR075987	Features	Location/Qualifiers				
AR075987	Source	1.1488				
AR075987	Source	/organism="unknown"				
AR075987	Source	/mol_type="unassigned DNA"				

ORIGIN

Query Match	83.6%	Score 979	DB 6	Length 1488
Best Local Similarity	92.2%	Pred. No. 8e-177	0	Indels 91
Matches 1080	Conservative	0	Mismatches	0
1	ATGAAGTCCCGCTTACCGCTGCGGACGACACACCTGTGGAAGGCAACTGGGCG	60		
350	ATGAAGTCCCGCTTACCGCTGCGGACGACACACCTGTGGAAGGCAACTGGGCG	409		
61	GTGATGCGGCGGCTGCTTACGACCGGCTCTGCGGCAACTGCTGCGGCTG	120		
410	GTGATGCGGCGGCTGCTTACGACCGGCTCTGCGGCAACTGCTGCGGCTG	469		
121	CTGCGCGCTGCGGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG	180		
470	CTGCGCGCTGCGGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG	529		
181	TTCTATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240		
530	TTCTATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	589		
241	CCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300		

Db 590 CCGGTGATGCTGCTGCTACGCTCAGAACCGGAGTCTGGGGTGGTGGCCCGGATTG 649
QY 301 GACAACTCGTGTGCAAGGCTTGCTTTCATGCTCTTTGGGCTCTCTGAGCA 360
Db 650 GAAACATCTGTGCAAGGCTTGCTTTCATGCTCTTTGGGCTCTCTGAGCA 709
QY 361 CTGCACTCTGAGCACTGAGCACTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTAC 420
Db 710 CTGCACTCTGAGCACTGAGCACTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTAC 769
QY 421 CGAGCGCACTACCTCTGAGCTGAGCGCACTGAGCGCTCTGAGCGCTCTTCTC 480
Db 770 CGAGCGCACTACCTCTGAGCTGAGCGCACTGAGCGCTCTGAGCGCTCTTCTC 829
QY 481 CTGAGCTTCTGAGCGCTACCTCTTTCATGAGGCTTGAGGAGTCTGAGCACTCTC 540
Db 830 CTGAGCTTCTGAGCGCTACCTCTTTCATGAGGCTTGAGGAGTCTGAGCACTCTC 889
QY 541 ACCGTGCTTTATTCAGATGATCAAGAGAGGCTCTGCTGCTGAGGATCTCT 600
Db 890 ACCGTGCTTTATTCAGATGATCAAGAGAGGCTCTGCTGCTGAGGATCTCT 949
QY 601 GTGCTTACTCTCACTCATGAGCTGCTGCTCTCTCTGCACTCTGAGCACTCTG 660
Db 950 GTGCTTACTCTCACTCATGAGCTGCTGCTCTCTCTGCACTCTGAGCACTCTG 1009
QY 661 GCGATGCGCACTCTATGAGATGCAACGAGGCTGAGGAGCACTCTGAGCACTCT 720
Db 1010 GCGATGCGCACTCTATGAGATGCAACGAGGCTGAGGAGCACTCTGAGCACTCT 1069
QY 721 AGGAGCTGTGCGAGCGCGCGCGAGACGAGAGGAAAGCTCTGAGCACTCTGAG 780
Db 1070 AGGAGCTGTGCGAGCGCGCGCGAGACGAGAGGAAAGCTCTGAGCACTCTGAG 1129
QY 781 CTGAGATCACTCTCTGCTGCTGAGCTGATGACCTGCTCTTCACTATGCTTCTG 840
Db 1130 CTGAGATCACTCTCTGCTGCTGAGCTGATGACCTGCTCTTCACTATGCTTCTG 1189
QY 841 GTAATTGCAATTGTCTGTGAGTCCCGGCAAGACCTGAGAGTGTGAGGCTTGA 900
Db 1190 GTAATT----- 1195
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QY 961 TAAAGATGTCAAGAGAAAAAGACCTTGAAGAGCAAGACCTCTGAGCTCTTGG 1020
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QY 1141 CAATTCCACTAATGAGATCCAGTCTGTGA 1171
Db 1399 CAATTCCACTAATGAGATCCAGTCTGTGA 1429

RESULT 2
AR371655 1488 bp DNA linear PAT 12-SEP-2003
LOCUS AR371655
DEFINITION Sequence 4 from patent US 6395499.
ACCESSION AR371655
VERSION AR371655.1 GI:34608648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1488)
AUTHORS Abramovitz,M., Metters,K., Bole,Y., Sawyer,N. and Slipetz,D.M.
TITLE Methods of identifying modulators of a DP prostaglandin receptor
JOURNAL Patent: US 6395499-A 4 28-MAY-2002;
FEATURES
source Location/Qualifiers
1..1488
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 83.6%; Score 979; DB 6; Length 1488;
Best Local Similarity 92.2%; Pred.No. 8e-177;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCCCGTTCATACCGCTGCGAGAACACACCTCTGTGAGAAAGGCAACTGGCG 60
Db 350 ATGAAGTCCCGTTCATACCGCTGCGAGAACACACCTCTGTGAGAAAGGCAACTGGCG 409
QY 61 GTGAGAGGCGGAGGCTCTTTCAGACACCGGCTCTTGGGCACTGTGAGCTCTGGGCTG 120
Db 410 GTGAGAGGCGGAGGCTCTTTCAGACACCGGCTCTTGGGCACTGTGAGCTCTGGGCTG 469
QY 121 CTGGCGCGCTCGAGGCTGAGGCTGAGCTGAGCGGCTCTGAGCGCTCTGAGCTG 180
Db 470 CTGGCGCGCTCGAGGCTGAGGCTGAGCTGAGCGGCTCTGAGCGCTCTGAGCTG 529
QY 181 TTCTACATGCTGT 240
Db 530 TTCTACATGCTGT 589
QY 241 CCGGTGATGCTGAGCTGCTGAGCTGAGAAACGAGAGTGTGAGGCTTGGCGCGGATTG 300
Db 590 CCGGTGATGCTGAGCTGCTGAGCTGAGAAACGAGAGTGTGAGGCTTGGCGCGGATTG 649
QY 301 GACAACTCGTGTGCGCAACCTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
Db 650 GACAACTCGTGTGCGCAACCTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 709
QY 361 CTGCACTCTGAGCACTGAGCACTGAGCTGAGCTCTCTCTTCTTCTTCTTCTTCTTCT 420
Db 710 CTGCACTCTGAGCACTGAGCACTGAGCTGAGCTCTCTCTTCTTCTTCTTCTTCTTCT 769
QY 421 CGAGCGCACTACCTCTGAGCTGAGCGCACTGAGCGCTCTGAGCGCTCTTCTCTC 480
Db 770 CGAGCGCACTACCTCTGAGCTGAGCGCACTGAGCGCTCTTCTCTCTCTCTCTCTC 829
QY 481 CTGAGCTTCTGAGCGCTACCTCTTTCATGAGGCTTCTGAGGCTTCTGAGGCTTCT 540
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QY 541 ACCGTGCTTTATTCAGATGATCAAGAGAGGCTCTGCTGCTGAGGCTTCTGAGGCT 600
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QY 661 GCGATGCGCACTCTATGAGATGCAACGAGGCTGAGGCTCTGAGGCTCTGAGGCT 720
Db 1010 GCGATGCGCACTCTATGAGATGCAACGAGGCTGAGGCTCTGAGGCTCTGAGGCT 1069
QY 721 AGGAGCTGTGCGAGCGCGCGCGAGACGAGAGGAAAGCTCTGAGCACTCTGAGAG 780
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QY 781 CTGAGATCACTCTCTGCTGCTGAGCTGATGACCTGCTCTTCACTATGCTTCTG 840
Db 1130 CTGAGATCACTCTCTGCTGCTGAGCTGATGACCTGCTCTTCACTATGCTTCTG 1189
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Db 1190 GTAATT----- 1195

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Query Match	72.3%	Score 847;	DB 6;	Length 1216;
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QY	61	GTGATGGCGCGGGGTGTCTTTTCAGACCGGCGCTCTGGGCAACCTGTGGCCCTGGGGCTG	120
Db	410	GTGATGGCGCGGGGTGTCTTTTCAGACCGGCGCTCTGGGCAACCTGTGGCCCTGGGGCTG	469
QY	121	CTGGCGCGGCTTGGGGGCTTGGGGTGTGTGTGTGGGGGTTCACACTGCGCCCGCTGGCCCTG	180
Db	470	CTGGCGCGGCTTGGGGGCTTGGGGTGTGTGTGTGGGGGTTCACACTGCGCCCGCTGGCCCTG	529
QY	181	TTCTACACATGTGGTGTGTGTGGGCTCTACAGGCTCACCGACTGTGCGGCAAGTGGCTCTTAAG	240
Db	530	TTCTACACATGTGGTGTGTGTGGGCTCTACAGGCTCACCGACTGTGCGGCAAGTGGCTCTTAAG	589
QY	241	CCGGT	300
Db	590	CCGGT	649
QY	301	GACAACTGT	360
Db	650	GACAACTGT	709
QY	361	CTGGCACTCTCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGG	420
Db	710	CTGGCACTCTCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGG	769
QY	421	CGAGCGCACATCACCCCTGTGGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	480
Db	770	CGAGCGCACATCACCCCTGTGGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	829
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QY	721	AGGGACTGT	780
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QY	781	CTGTGATCAACCTCTGT	840
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DEFINITION	Human DP prostanoïd receptor (PTGDR) gene, 5' region and partial cds.		
ACCESSION	U31332		
VERSION	U31332.1	GI:940378	
KEYWORDS	.		

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1216)
 AUTHORS Boie,Y., Sawyer,N., Slipeitz,D.M., Wetzers,K.M. and Abramovitz,M.
 TITLE Molecular cloning and characterization of the human prostanoid DP receptor
 JOURNAL J. Biol. Chem. 270 (32), 18910-18916 (1995)
 MEDLINE 95370201
 PUBMED 7642548
 REFERENCE 2 (bases 1 to 1216)
 AUTHORS Abramovitz,M. and Boie,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1995) Mark Abramovitz, Biochemistry and Molecular Biology, Merck Frost Center for Therapeutic Research, P.O. Box 1005, Pointe Claire Dorval, Quebec H9R 4P8, Canada
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 CSLPVI"
 1196. .>1216
 ORIGIN
 Intron
 Query Match 72.3%; Score 847; DB 9; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 1.3e-151;
 Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAGTCCGCGCTTCAACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTGGCG 60
 DB 350 ATGAAGTCCGCGCTTCAACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTGGCG 409
 QY 61 GTGATGGGCGGGGTGCTCTTACAGACCGGCTCTGGGCAACCTGTGGCGCTG 120
 DB 410 GTGATGGGCGGGGTGCTCTTACAGACCGGCTCTGGGCAACCTGTGGCGCTG 469
 QY 121 GTGGCGCGCTGGGGGTGCTGTCTCGCGCGTCCACTGTGCGCGCTCGCTCGCTC 180
 DB 470 GTGGCGCGCTGGGGGTGCTGTCTCGCGCGTCCACTGTGCGCGCTCGCTCGCTC 529
 QY 181 TTCTAATGCTGT 240
 DB 530 TTCTAATGCTGT 589
 QY 241 CCGGT 300
 DB 590 CCGGT 649
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 DB 650 GACAACTCGT 709
 QY 361 CTGCAACTCTGTGGCATGTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 710 CTGCAACTCTGTGGCATGTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769

QY 421 CGACGCAATCAACCTGTGGCGCTGTGGCGCATGTGTGGCGCGCGGTGTGTGGCGCTTCTCC 480
 DB 770 CGACGCAATCAACCTGTGGCGCTGTGGCGCATGTGTGGCGCGCGGTGTGTGGCGCTTCTCC 829
 QY 481 CTGCGCTTGTGGCGCGCTGTGGCGCTGTGGCGCATGTGTGGCGCGCGGTGTGTGGCGCG 540
 DB 830 CTGCGCTTGTGGCGCGCTGTGGCGCTGTGGCGCATGTGTGGCGCGCGGTGTGTGGCGCG 889
 QY 541 ACCTGT 600
 DB 890 ACCTGT 949
 QY 601 GTGCTTGT 660
 DB 950 GTGCTTGT 1009
 QY 661 GCGATGCGCACTCTGT 720
 DB 1010 GCGATGCGCACTCTGT 1069
 QY 721 AGGACGT 780
 DB 1070 AGGACGT 1129
 QY 781 CTGATCACTCTGT 840
 DB 1130 CTGATCACTCTGT 1189
 QY 841 GTATTG 847
 DB 1190 GTATTG 1196

RESULT 6
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 LOCUS Homo sapiens chromosome 14 clone RP11-221n7 map 14, WORKING DRAFT
 DEFINITION
 ACCESSION AC012407
 VERSION AC012407.4
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 14, clone RP11-221n7
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckert,R., Boguslavsky,L., Bouhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Dominko,M., Donegan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karates,A., Klein,J., Lehoczy,J., Lien,C., Locke,K., MacDonald,P., Margulis,N., McEwan,P., McGuirk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Turrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Bede,F., Boguslavsky,L., Bouhgalter,B., Brown,M., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,

TITLE
JOURNAL

COMMENT

Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardy, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Grant, G., Hages, B., Heatford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Laroque, K., Lamazares, R., Landers, T., Lebecky, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPeckers, R., Melidim, J., Menus, L., Miho, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Plesni, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 16, 2000 this sequence version replaced gi:8096911.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L2358

Center clone name: 221_N7

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 142459 bases at least Q40

Consensus quality: 149548 bases at least Q30

Consensus quality: 152199 bases at least Q20

Insert size: 168000; agarose-fp

Insert size: 154308; sum-of-contigs

Quality coverage: 3.4 in Q20 bases; agarose-fp

Quality coverage: 3.7 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1      1127: contig of 1127 bp in length
*      1128: gap of 100 bp
*      1228: contig of 1068 bp in length
*      2296: gap of 100 bp
*      2396: contig of 1093 bp in length
*      3489: gap of 100 bp
*      3589: contig of 1419 bp in length
*      5008: gap of 100 bp
*      5107: gap of 100 bp
*      5108: contig of 2015 bp in length
*      7123: gap of 100 bp
*      7223: gap of 100 bp
*      7223: contig of 1427 bp in length
*      8649: gap of 100 bp
*      8650: gap of 100 bp
*      8650: contig of 2533 bp in length
*      11283: gap of 100 bp
*      11283: contig of 2787 bp in length
*      11383: gap of 100 bp
*      14169: contig of 1510 bp in length
*      14270: gap of 100 bp
*      14270: contig of 1510 bp in length
*      15879: gap of 100 bp
*      15880: contig of 2605 bp in length
*      15880: gap of 100 bp
*      18485: gap of 100 bp
*      18485: contig of 3990 bp in length
*      22574: gap of 100 bp
*      22575: gap of 100 bp

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FEATURES

source

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22675      26492: contig of 3818 bp in length
*      26493      26592: gap of 100 bp
*      26493      30305: contig of 3713 bp in length
*      30306      30405: gap of 100 bp
*      30406      33575: contig of 3170 bp in length
*      33576      33675: gap of 100 bp
*      33676      36681: contig of 2906 bp in length
*      36682      40759: contig of 4078 bp in length
*      40760      40859: gap of 100 bp
*      40860      47200: contig of 6341 bp in length
*      47201      47201: gap of 100 bp
*      47301      57681: contig of 10381 bp in length
*      57682      57781: gap of 100 bp
*      57782      65982: contig of 8201 bp in length
*      65983      66082: gap of 100 bp
*      66083      75420: contig of 9338 bp in length
*      75421      75520: gap of 100 bp
*      75521      85239: contig of 9719 bp in length
*      85240      85339: gap of 100 bp
*      85340      98725: contig of 13386 bp in length
*      98726      98825: gap of 100 bp
*      98826      110171: contig of 11346 bp in length
*      110172      110271: gap of 100 bp
*      110272      123829: contig of 13558 bp in length
*      123830      123929: gap of 100 bp
*      123930      136463: contig of 12534 bp in length
*      136464      136563: gap of 100 bp
*      136564      156808: contig of 20245 bp in length.

FEATURES
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2396..3488
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85340..98725
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110272..123829
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Best Local Similarity 100.0%; Pred. No. 1e-151;
Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 89185 ATGAAGTCCGCTTCTACCGCTGCGCCAGAACACCACTCTGTGAAAAGCACTGGCG 89126
QY 61 GTGATGGGCGGGGCTCTTACAGCACCGGCTCTGGGCAACTGCTGGGCGCTG 120
DB 89125 GTGATGGGCGGGGCTCTTACAGCACCGGCTCTGGGCAACTGCTGGGCGCTG 89066
QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTCTGCGCGCTGCACTGGCGCGCTGCTGCTG 180
DB 89065 CTGGCGCGCTCGGGGCTGGGGTGTGTCTGCGCGCTGCACTGGCGCGCTGCTGCTG 89006
QY 181 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 89005 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 88946
QY 241 CCGGGGCTGCTGGCTGCTACGCTGCAAGACCGGAGCTGGGGGCTGCGCGCGGCTG 300
DB 88945 CCGGGGCTGCTGGCTGCTACGCTGCAAGACCGGAGCTGGGGGCTGCGCGCGGCTG 88886
QY 301 GACAACTCGTTGTGCGCAAGCTTGGCTTCTTATGCTTCTTGTGGGCTCTCTGACA 360
DB 88885 GACAACTCGTTGTGCGCAAGCTTGGCTTCTTATGCTTCTTGTGGGCTCTCTGACA 88826
QY 361 CTGCAACTCTGCGCCATGCGACTGAGTGTGCTCTCTTGAAGGCACTTCTTCTAC 420
DB 88825 CTGCAACTCTGCGCCATGCGACTGAGTGTGCTCTCTTGAAGGCACTTCTTCTAC 88766
QY 421 CGACGGCAATACACCTGCGGCTGGGGGCGCACTGGTGGCCCGGCTGGTGAAGCGCTTCTG 480
DB 88765 CGACGGCAATACACCTGCGGCTGGGGGCGCACTGGTGGCCCGGCTGGTGAAGCGCTTCTG 88706
QY 481 CTGGCTTCTGCGCGCTACCTTTCATGAGGCTTGGAGAGTTCGTGCACTGACCCCGGCG 540
DB 88705 CTGGCTTCTGCGCGCTACCTTTCATGAGGCTTGGAGAGTTCGTGCACTGACCCCGGCG 88646
QY 541 ACCTGGTCTTATTCAGATGCTTCAGAGAGAGAGGCTCGTGTGCTGGGGTACTCT 600
DB 88645 ACCTGGTCTTATTCAGATGCTTCAGAGAGAGAGGCTCGTGTGCTGGGGTACTCT 88586
QY 601 GTGCTCTACTCAAGCTCAATGCGGCTGCTGCTTGGCAACCGTGTGCAACCTCGGCG 660
DB 88585 GTGCTCTACTCAAGCTCAATGCGGCTGCTGCTTGGCAACCGTGTGCAACCTCGGCG 88526
QY 661 GGCATGCGCAACTCTATGCACTGCACTGCGGCGCTGCACTGCGGCTCTGCGAC 720
DB 88525 GGCATGCGCAACTCTATGCACTGCACTGCGGCGCTGCACTGCGGCTCTGCGAC 88466
QY 721 AGGGAAGTGTGCGAGCGCGCGCGGAGACGGAGGAAAGCTTCCCTCAGCCCTGAGAGAG 780
DB 88465 AGGGAAGTGTGCGAGCGCGCGCGGAGACGGAGGAAAGCTTCCCTCAGCCCTGAGAGAG 88406

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QY 781 CTGATACCTCTCTGCTGCGGCTGATGACCGGCTCTTCACTATGATGTTCTGCCC 840
DB 88405 CTGATACCTCTCTGCTGCGGCTGATGACCGGCTCTTCACTATGATGTTCTGCCC 88346
QY 841 GTTATTG 847
DB 88345 GTTATTG 88339

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RESULT 7

CNS05TF6/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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JOURNAL

AUTHORS

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JOURNAL

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STS

FEATURES

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/db_xref="taxon:9606"

/chromosome="14"

/clone="R-452D12"

/clone_lib="RPC1-11"

43692..44026

/note="matching EMBL:U19487"

Percentage of bases with a quality value >= 40 : 99 %.

Location/Qualifiers

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/mol_type="genomic DNA"

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43692..44026

/note="matching EMBL:U19487"

Percentage of bases with a quality value >= 40 : 99 %.

Location/Qualifiers

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 dbSTS: STS22645
 identified using the e-PCR software (G. Schuler)
 96853..97026
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 RHD: RH71220
 dbSTS: STS0986
 identified using the e-PCR software (G. Schuler)
 98037..98222
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 RHD: RH92017
 dbSTS: STS65021
 identified using the e-PCR software (G. Schuler)"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1e-151;
 Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCCGCTTCTACCGCTGCGCAACACCACTCTGTGGAAAAAGCACTCGCG 60
 DB 103968 ATGAAGTCCGCTTCTACCGCTGCGCAACACCACTCTGTGGAAAAAGCACTCGCG 103909
 QY 61 GTGATGGCGGGGCTCTTCAAGACCGGCTCTCTGGGCAACTGCTGGCCCTGGGGCTG 120
 DB 103908 GTGATGGCGGGGCTCTTCAAGACCGGCTCTCTGGGCAACTGCTGGCCCTGGGGCTG 103849
 QY 121 CTGGCGCGCTCGGGGCTGGGGGCTGCTGCGCGGCTCACTGCGCGCGCTCGGCTG 180
 DB 103848 CTGGCGCGCTCGGGGCTGGGGGCTGCTGCGCGGCTCACTGCGCGCGCTCGGCTG 103789
 QY 181 TTCTACATCTGGTGTGTGGCTGACGCTCACCAGCTTGTGTGGCAAGTCCCTCTTAAC 240
 DB 103788 TTCTACATCTGGTGTGTGGCTGACGCTCACCAGCTTGTGTGGCAAGTCCCTCTTAAC 103729
 QY 241 CCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 103728 CCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 103669
 QY 301 GACAACTCGTGGGCAAGGCTTGGCTTCTCATGCTTCTTGGGGCTCTCTCGACA 360
 DB 103668 GACAACTCGTGGGCAAGGCTTGGCTTCTCATGCTTCTTGGGGCTCTCTCTCGACA 103609
 QY 361 CTGCACTCTCGGCGCATGCGACTGAGTGTGCTCTCTCTAGGAGCACTTCTTCTAC 420
 DB 103608 CTGCACTCTCGGCGCATGCGACTGAGTGTGCTCTCTCTAGGAGCACTTCTTCTAC 103549
 QY 421 CGACGCGCATCATACCTGCGGCTGGCGGCACTGTGGCCCGGCTGGTGAAGCGCTTCTC 480
 DB 103548 CGACGCGCATCATACCTGCGGCTGGCGGCACTGTGGCCCGGCTGGTGAAGCGCTTCTC 103489
 QY 481 CTGGCTTCTGGCGGCTTACCTTTCATGAGGCTTGGGAAAGTGTGAGACTGCTCCCGG 540
 DB 103488 CTGGCTTCTGGCGGCTTACCTTTCATGAGGCTTGGGAAAGTGTGAGACTGCTCCCGG 103429
 QY 541 ACCTGGTCTTTATCCAGATGTCTCAAGAGAGGCTGCTGTGCTGCTGGGATCTCT 600
 DB 103428 ACCTGGTCTTTATCCAGATGTCTCAAGAGAGGCTGCTGTGCTGCTGGGATCTCT 103369
 QY 601 GTGCTTACTCCAGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 103368 GTGCTTACTCCAGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 103309
 QY 661 GGCATGCGCACTCTATGCGAGTGAACGCGGCTGCGAGGAGACCGCGGCTCTGACAC 720
 DB 103308 GGCATGCGCACTCTATGCGAGTGAACGCGGCTGCGAGGAGACCGCGGCTCTGACAC 103249
 QY 721 AGGACTGTGCGGAGCGCGCGCGAGCGAGAGGAGAGCGTCCCTCAGCCCTCTGAGAG 780
 DB 103248 AGGACTGTGCGGAGCGCGCGCGAGCGAGAGGAGAGCGTCCCTCAGCCCTCTGAGAG 103189
 QY 781 CTGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

DB 103188 CTGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 103129
 QY 841 GTGATG 847
 DB 103128 GTGATG 103122

RESULT 8
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 LOCUS Human chromosome 14 DNA sequence BAC R-262M8 of library RCI-11
 DEFINITION from chromosome 14 of Homo sapiens (human), complete sequence.
 ACCESSION AL355833
 VERSION AL355833.4 GI:13990340
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 197817)
 JOURNAL Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Winkler, P., Brotier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Bruls, T., deBardinis, V., Cruaud, C., Gyapay, G., Saurin, M. and Weissenbach, J.
 REFERENCE Unpublished
 TITLE 2 (bases 1 to 197817)
 JOURNAL Genoscope.
 AUTHORS Direct Submision
 REFERENCE Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
 TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 JOURNAL - Web : www.genoscope.cns.fr)
 COMMENT On May 7, 2001 this sequence version replaced gi:13897294.

COMMENT
 Genoscope / Centre National de Sequencage
 Center: Genoscope / Centre National de Sequencage
 Web site: http://www.genoscope.cns.fr/
 Contact: Sequef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-452D12
 Downstream BAC (overlapping the SP6 end) : R-933I1 (AC=AL157971)

----- Summary Statistics
 Assembly program: Phrap; version 2.0
 Quality coverage: 8.90x in Q20 bases; sum-of-contigs

----- Overall quality chart :
 Range : bases
 0 : 2
 1 - 9 : 4
 10 - 19 : 41
 20 - 29 : 112
 30 - 39 : 876
 40 - 49 : 4041
 50 - 59 : 8035
 60 - 69 : 5759
 70 - 79 : 10473
 80 - 89 : 37260
 90 - 99 : 131214

Percentage of bases with a quality value >= 40 : 99 %.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="R-262M8"
 /clone_1lb="RPCT-11"
 100237..100571
 /note="matching EMBL:U19487
 RHD: RH9028

FEATURES

source

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Identified using the e-PCR software (G. Schuler)"
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RHHB:RH71220
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154580..154765
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RHHB:RH92017
dbSTS:STS65021
Identified using the e-PCR software (G. Schuler)"

ORIGIN
Query Match 72.3%; Score 847; DB 9; Length 197817;
Best Local Similarity 100.0%; Pred. No. 1e-151;
Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGCTTCTACCGCTGCGAGAACCACTCTGTGAAAAAGCAACTCGCG 60
DB 160510 ATGAAGTCGCGCTTCTACCGCTGCGAGAACCACTCTGTGAAAAAGCAACTCGCG 160451
QY 61 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGGGCGCTG 120
DB 160450 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGGGCGCTG 160391
QY 121 CTGGCGCGCTCGGGGGCTGGGGGGTGTCTGGGGCTTCACTGGGCGCGCTGGGTC 180
DB 160390 CTGGCGCGCTCGGGGGCTGGGGGGTGTCTGGGGCTTCACTGGGCGCGCTGGGTC 160331
QY 181 TTCTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
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DB 160270 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 160211
QY 301 GACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 160210 GACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 160151
QY 361 CTGCAACTCTGCGCGAGCACTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 160150 CTGCAACTCTGCGCGAGCACTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 160091
QY 421 CGACGGCAATCACTCTGCGCGCTGGGGCGCACTGTGTGTGTGTGTGTGTGTGTGT 480
DB 160090 CGACGGCAATCACTCTGCGCGCTGGGGCGCACTGTGTGTGTGTGTGTGTGTGT 160031
QY 481 CTGGCTTCTGGCGGCTACCTTTCATGGGGCTTGGGAAAGTTGGTGAAGTACCTCC 540
DB 160030 CTGGCTTCTGGCGGCTACCTTTCATGGGGCTTGGGAAAGTTGGTGAAGTACCTCC 159971
QY 541 ACCTGTGTCTTATCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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QY 781 CTGATCATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 159730 CTGATCATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 159671

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QY 841 GTAAATG 847
DB 159670 GTAAATG 159664

RESULT 9
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DEFINITION Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.
ACCESSION U92289
VERSION U92289.1 GI:2459674
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1315)
AUTHORS Geraschenko,D., Beuckmann,C.T., Kanaoka,Y., Eguchi,N.,
Gordon,W.C., Urade,Y., Bazan,N.G. and Hayashi,O.
TITLE Dominant expression of rat prostanoic acid receptor mRNA in
epithelium, and ciliary processes
JOURNAL J. Neurochem. 71 (3), 937-945 (1998)
MEDLINE 98387174
PUBMED 9721719
REFERENCE 2 (bases 1 to 1315)
AUTHORS Geraschenko,D., Kanaoka,Y., Beuckmann,C. and Urade,Y.
TITLE Direct Substitution
JOURNAL Submitted (07-MAR-1997) Molecular Behavioral Biology, Osaka
BioScience Institute, 6-2-4 Furendai, Suita, Osaka 565, Japan
FEATURES
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AFCALEPFAFGKRFVYCPGTWCFIOMIHKRSFVSIGFVLSLMALLVLAIVNCL
GAMSLYAMHRRORHHPRCSDRPAOSGSDYHRSBPLEEDHFLVLLALTVLFTMC
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ORIGIN
Query Match 47.5%; Score 556; DB 10; Length 1315;
Best Local Similarity 71.2%; Pred. No. 4.9e-96;
Matches 830; Conservative 0; Mismatches 230; Indels 106; Gaps 3;

QY 12 GTTTCACGCTGCCAGAACCACTCTGTGAAAAAGCAACTCGCGGTGATGGCGG 71
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QY 72 GGTGCTTTCAGACCGGCTCTGGGCAACTGTGCGGCTGGGGCTGTGGCGGCTC 131
DB 129 TGTGCTTTCAGACCGGCTCTGGGCAACTGTGCGGCTGGGGCTGTGGCGGCTC 188
QY 132 GGGGCTGGGGGTGTCTCGCGGCTCTCACTGGCGCGCTGGCGCTTCTTACATGCT 191
DB 189 CGGGGCTGGGGGTCTGTGGCGGCACTGGATCGCGCGCTGGCTTTTATGTGCT 248
QY 192 GGTGTGTGCTGACGCGTACCGACTTGTGGGCAAGTCTCTTACGCGCGGTGCT 251
DB 249 AGTGTGCGGCTTACGCGTACCGACTTGTGGGCAAGTCTCTTACGCGCGGTGCT 308

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OY 252 GGCTGCTTCAAGCTCAGAACCGAGAGTCTGGGGTCTTGGCCCGCATTTGGACAATCGTT 311
DB 309 GGCTGCTTCAAGCTCAGAACCGAGAGTCTGGGGTCTTGGCCCGCATTTGGACAATCGTT 368
OY 312 GTGCCAAGCTTGGCTTCTTCAATGCTTCTTGGGGTCTCTCGACACTGCAATCGCT 371
DB 369 ATGTGAAGCTTGGCTTCTTCAATGCTTCTTGGGGTCTCTCGACACTGCAATCGCT 428
OY 372 GGCCATGAGCACTGAGTGTGCTCTCCCAAGGGGACCTTTCTTCAACGAGCAAT 431
DB 429 GGCTATGAGCACTGAGTGTGCTCTCCCAAGGGGACCTTTCTTCAACGAGCAAT 488
OY 432 CACCTGCGCTGGGCGCAGCTGTGCGCCGAGTGTGAGCGCTTCTCCCTGGCTTCTG 491
DB 489 CACCGCGCGCTGGGCGCAGCTGTGCGCCGAGTGTGAGCGCTTCTCCCTGGCTTCTG 548
OY 492 CGCGCACTTTCATGAGGCTTGGGAGTTCGCGCACTGCTGCGCGGACCTGGGCT 551
DB 549 TGGGCTCCCTTGTGCTGGGAGTTCGCGCACTGCTGCGCGGACCTGGGCT 608
OY 552 TATCCAGATGATCCAGAGAGGCTCGCTGTGCTGAGGCTTCTGTGCTTACTC 611
DB 609 CATCCAGATGATCCAGAGAGGCTCATTTCTGATTAAGCTTCTGTGCTTACTC 668
OY 612 CAGCTCATGAGGCTGCTGCTCTGCTCCACCGTGTGTGCACTTGGCGCATGCGCAA 671
DB 669 CAGCTCATGAGGCTGCTGCTCTGCTCCACCGTGTGTGCACTTGGCGCATGCGCAA 728
OY 672 CCTCATGAGTGCACCGGCGGCTGAGAGGACCGCGGCTCTGTGACCAAGGACCTGTG 731
DB 729 CCTCATGAGTGCACCGGCGGCTGAGAGGACCGCGGCTCTGTGACCAAGGACCTGTG 788
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DB 789 CGAGTGAAGCTGACATGAGAGGAGTGGTCCCGAATCTTTGAGAGAGTGGACCACT 848
OY 792 CCGTCTGAGGCTGATGACCGTGTCTTCACTATGTGTCTTCTGCGGTAATGCAAT 851
DB 849 TGTTCGTGAGGCTCTGACGACAGTGTCTTCACTATGTGTCTTCTGCGGTAAT 903
OY 852 TGTTCGTGAGGCTCTGACGACAGTGTCTTCACTATGTGTCTTCTGCGGTAAT 911
DB 904 ----- 903
OY 912 GTGCTGCTCTCTCTTCTTCCCAAGTATGCGCTTACTATGAGCAATTAAGATGCA 971
DB 904 -----TATGTGCTTACTATGAGCTTTAACTGT-- 935
OY 972 AGGAGAAAAAGAGACCTTGAAGAAAGCAAGACCTCGAGCTTGGCAATTTCTATCTG 1031
DB 936 -----GGAACAGAGCTGACGAGAGCTCGAAGACCTCCAAAGCTTGGCTTCTGCTG 988
OY 1032 TGATTTCAATGAGACCTTGAATTTTATCATTTTTCAGATTCCTCAGATTTCCGATAT 1091
DB 989 TGATTTCAATGAGACCTTGAATTTTATCATTTTTCAGATTTCCGATAT 1048
OY 1092 TTTTTCACAAGATTTTATTAAGCTCTTAAGTACAGAGCGGATGACAGATTC-- 1147
DB 1049 TATTTTCAAGAGTTTTCACAAGAGCTCTGATCTACAGAAACTGTGTGACGATTTCTGGC 1108
OY 1148 --ACTTAACATGGAATCAAGTCTGTGA 1171
DB 1109 AGACTTAACATGGAATCAAGTCTGTGA 1134

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RESULT 10
AF120101 1074 bp mRNA linear ROD 10-AUG-2000
LOCUS AF120101
DEFINITION Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.
ACCESSION AF120101
VERSION AF120101.1 GI:4567037
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE

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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Wright,D.H., Nanel,F., Metters,K.M. and Ford-Hutchinson,A.W.
TITLE A novel biological role for prostaglandin D2 is suggested by
distribution studies of the rat DP prostanoid receptor
JOURNAL Eur. J. Pharmacol. 377 (1), 101-115 (1999)
MEDLINE 99376163
PUBMED 10448933
REFERENCE 2 (bases 1 to 1074)
AUTHORS Wright,D.H. and Abramowitz,M.
TITLE Direct Submision
JOURNAL Submitted (13-JAN-1999) Biochemistry and Molecular Biology, Merck
Frost Centre for Therapeutic Research, P.O. Box 1005, Pointe
Claire - Dorval, Quebec H9R 4P8, Canada
FEATURES
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GAMSNLYAMHRRORHPRCSRDRAQSSDYHSGSPNLELDHVLALITVLFPMC
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ORIGIN
Query Match 47.3%; Score 554.4; DB 10; Length 1074;
Best Local Similarity 71.1%; Pred. No. 1e-95;
Matches 829; Conservative 0; Mismatches 231; Indels 106; Gaps 3;
OY 12 GTTCTACGCGTCCAGAACACCACTCTGTGAAAAAGCAACTGCGCGTATGCGCG 71
DB 9 GTCTTACGCTCTCTGAGGACGACCTGAGTGAACGCGGCTCTCTGAGCAATAGGTG 68
OY 72 GGTGCTCTTCAACACCGGCTCTGCGGCAACTGTGCGGCGCTGGGGCTGCGCGCTC 131
DB 69 TGTGCTTCAATGAGAGACTGTGGCAACTCTGCGCTGTGTCTGTGGCGGATC 128
OY 132 GCGGCTGGGAGTGTCTGCGGCGTCACTGCGCGCTGCGCGCTGCTTCTTCAATGCT 191
DB 129 CGGGCTGGGAGTCTGTGCGGCGCAAGCTGATCGCGCGCTGCTTTTATGATGCT 188
OY 192 GGTGTGTGCTGAGCGGTACCGACTTGTGGGCAAGTCTCTTCAAGCCGCGTGTCT 251
DB 189 AGTGTGCGGCTTGAAGAGTACCGACTGTGCGGCAAGTCTCTGATCAGCCGATGTCT 248
OY 252 GGCTGCTAAGCTCGAAGACCGAGTGTGCGGAGTGTGCGCGCGGATGAGCAATCGTT 311
DB 249 GGCTGATAGCGGCAAAATGAGAGCTTAAGAAATGCTGCTGCTCGCTCAGGACCACTT 308
OY 312 GTGCCAAGCTTGGCTTCTTCAATGCTCTTTGGGCTCTCTCGACACTGCAATCTCT 371
DB 309 ATGTGAAGCTTGGCTTCTTCAATGCTCTTTGGGCTTCTTGGGCTTCTTCAAGTACT 368
OY 372 GGCCATGAGCACTGAGTGTGCTCTCCCAAGGGGACCTTTCTTCAACGAGCAAT 431
DB 369 GGCTATGAGCACTGAGTGTGCTCTCCCAAGGGGACCTTTCTTCAACGAGCAAT 428
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Db 765 CCAAGTCAGGCTCAGACTACAGGACGCGGTCCTGATCCTTTGGAGAGCTGACCACTT 824
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Qy 852 TGTTCCTGAGTCCCGCCAGACACCTGGAGTAGTGAAGCTTGAAGAAACATTTTCA 911
Db 880 ----- 879
Qy 912 GTGCTGCTCTCTCTCTTCTCTCCAAATATCGGCTTACTATGAGACATTTAAGATGTCA 971
Db 880 -----TATCGTGGACTATGAGACCTTTAAACCTTG----- 910
Qy 972 AGAGAAAAACAGACCTCTGAGAGACAGAAAGACCTCGAGCTTGCAATTTCTATCTG 1031
Db 911 -----AGAACAAAGCTGAAGAGACTGAGAGACCTCCAGCTTGCGTTCTCTCTG 964
Qy 1032 TGAATTCATTTGTGACCCCTTGATTTTATCATTTTTCAGATCTCGATTTTGGATAT 1091
Db 965 TGAATTTCCATGAGGACCCCTGGATCTTCATCATCTTCAAGACTTCAGTATTCGGATGT 1024
Qy 1092 TTTTTCACAAAGTTTTCATTTAGCTCTTAAGTACGAGACCGGTGACCAATTC----- 1147
Db 1025 TATTTTCACAAAGTTTTCACAAAGCTCTGATCTTACAGAACTGGAGCAGCAATTCACAGC 1084
Qy 1148 --ACTAACATGGAATCCAGTCTGTGA 1171
Db 1085 AAGTAACTGGAAATCACTTTGTGA 1110

RESULT 12
E10039 1071 bp RNA linear PAT 29-SEP-1997
LOCUS Base sequence of the open leading frame of prostaglandin D
DEFINITION receptor.
E10039

ACCESSION E10039.1 GI:22026661
VERSION JP 1995258295-A/1.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1071)
AUTHORS Ichikawa,A., Nakao,I. and Narumiya,S.
TITLE PROSTAGLANDIN D RECEPTOR, ITS PRODUCTION, DNA ENCODING THE SAME
RECEPTOR, VECTOR COMPRISING THE SAME DNA AND HOST TRANSFORMED WITH
THE SAME VECTOR
JOURNAL Patent: JP 1995258295-A 1 09-OCT-1995;
ONO PHARMACEUT CO LTD

COMMENT OS Mus.sp. (mouse)
PN JP 1995258295-A/1
PD 09-OCT-1995

PF 22-MAR-1994 JP 1994075382
PI ICHIKAWA ATSUSHI, NAKAO ICHIKAZU, NARUMIYA SHU PC
C07K14.7/05, C12N5/10, C12N15/09, C12P21/02//A61K8/00, C12P21/02, PC
C12R1(91);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..1071
FT /organism='Mus sp.'
FT /tissue='Lung'.
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Location/Qualifiers
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ORIGIN

Query Match 47.2%; Score 552.8; DB 6; Length 1071;
Best Local Similarity 71.2%; Pred. No. 2e-95;
Matches 809; Conservative 0; Mismatches 227; Indels 100; Gaps 2;

Qy 12 GTTCTACCGCTCCAGAACACCACCTGTGTGAAAAAGGCAATCGCGGTGATGGCGG 71
Db 9 GTCTATGCTGTCAAGACATTCACCTGGGTGAAAGGGGCTCTCGGCGACATGGGCGC 68
Qy 72 GGTGCTCTTACAGACCGGCTCTTGAGCAACTGTGAGCCCTGAGGCTCTGCGCGCTC 131
Db 69 TGTGCTCTTGGGTGGGGGCTTCTGGGCAATCTTCTGGGCTGTGTGCTGCGCGCTC 128
Qy 132 GGGGCTGGGGGTGTGTGCGCGGCTGCACTGGCGCGCTGCTGCTGTCTTCAATGCT 191
Db 129 GGAATCTGGGCTTGTGCGGCGCAGGGCCTTACACCGCGCGCTGCTTATGTGCT 188
Qy 192 GGTGTGTGCTGACGCTGACCGATTCGCTGTGGGCAAGTGCCTTAAGCCGAGTGTCT 251
Db 189 CGTGTGTGCTTGAAGGTCAACCGATCTGTGGCAAGTGTGTGATCAGCCGATGCTCT 248
Qy 252 GGTGCTTACGCTCAAGAACCGAGTCTGGGGTCTTGGCGCCGCAATGGAACATCGTT 311
Db 249 GGTGCTTACGCGCAAAACCAAGGCTTAAGGAACTGTGCTGCTCAGGCAATCAGTT 308
Qy 312 GTGCCAAGCCTTGCGCTTCTGATGCTCTTGGGCTCTGCTGCACTGCAATCTCT 371
Db 309 ATGCAAACTGTGCGCTTCTGATGCTCTTGGGCTGAGCTTGAACCTTACACTGTT 368
Qy 372 GGCATGCGCACTGAGTGTGCTCTCCCTAGGGCAACCTTCTTCTTACCAAGGCAAT 431
Db 369 GGTATGCGGTGAGTGTGCTGTCTGTGGGACACCCCTTCTTACCAAAAGGCACT 428
Qy 432 CACCTGCGCTGGGGGCACTGTGTGCCCGGTGTGAGCGCTTCTCCCTGCTTTCTG 491
Db 429 CACTTGGCGCGGGGAGTGTGTGTGACACCGGTGTGTGGCGCGCTTGTGTGGCTTTCTG 488
Qy 492 CGCGTACCTTTCATGGGCTTGAGGAAGTGTGTGCACTGCTCCCGGCACTGTGCTT 551
Db 489 TGGGCTCCCTTGTGCTGCTTGTGGAAAGTTCGTGCACTGTCCAAGGCACTGTGTT 548
Qy 552 TATCAGATGTCCAAGAGAGGCTCGCTGTGCTGTGGGTACTGTGCTCTACTC 611
Db 549 CATCAGATGATCCAAGAGAGCGTTCAATTTGGAATAGGCTTCTGTGCTCTACTC 608
Qy 612 CAGCTCATGGGCTGTGTGTCTTGTGCAACCGTGTGTGCAACCTGCGGCAATCGGCA 671
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Qy 672 CCTATGAGATGCAACCGGCTGAGCGGCAACCGGCTCTCTCACCAGGAGTGTGTC 731
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Qy 732 CGAGCGCGCGGGAACGGAGGAAAGCTCCCTCAGCCCTGAGAGAGTGTGATCACT 791
Db 729 CCAATCAGGCTCAGACTACAGGAGCGGCTCTGATCTTTGGAGAGTGTGACACTT 788
Qy 792 CCGTGTGCTGCGGCTGATGACCGGTGTCTTCACTATGTGTCTGCGCCGTAATGCAAT 851
Db 789 TGTGCTGCTGCTGTCTATGACAGTGTCTTCACTATGTGTCTGCGCTTAAATTT----- 843
Qy 852 TGTTCCTGAGTCCCGCCAGACACTGGAGTGTGAGGCTTGAAGAAACATTTTCA 911
Db 844 ----- 843
Qy 912 GTGCTGCTCTCTCTCTTCTCCAAATATCGGCTTACTATGAGACATTTAAGATGTCA 971
Db 844 -----TATCGTGGACTATGAGACCTTTAAACCTTG----- 874
Qy 972 AGAGAAAAACAGACCTCTGAGAGACAGAAAGACCTCGAGCTTGCGATTTCTATCTG 1031
Db 875 -----AGAACAAAGCTGAAGAGACTGAGAAAGACCTCCAGCTTGGCTTCTCTGCTG 928
Qy 1032 TGAATTCATTTGTGACCCCTTGATTTTATCATTTTTCAGATCTCGAATTTTGGATAT 1091
Db 929 TGAATTTCCATGAGGACCCCTGATCTTCATCATCTTCAAGACTTCAAGTATTCGGATGT 988

Qy 1092 TTTTTCACAGATTTTCATTAGACCTTTAGTACAGAGACCGGTGACGAATTC 1147
Db 989 TATTTCACAGAGTTTTCACAGACCTTGTATCTACAGAACTGGAGACGCAATTC 1044

RESULT 13

LOCUS D29764S1 895 bp DNA linear ROD 12-OCT-2002
DEFINITION Mus musculus gene for prostaglandin D receptor, exon 1.
ACCESSION D29764
VERSION D29764.1 GI:577718

KEYWORDS 1 of 2
SEGMENT
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 895)
Hirata, M., Kakizuka, A., Aizawa, M., Ushikubi, F. and Narumiya, S.

TITLE Molecular characterization of a mouse prostaglandin D receptor and
functional expression of the cloned gene

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (23), 11192-11196 (1994)
MEDLINE 95062232
PUBMED 7972033

REFERENCE 2 (bases 1 to 895)
AUTHORS Hirata, M.
TITLE Direct Submission
SUBMITTED (01-APR-1994) Masakazu Hirata, Faculty of Medicine, Kyoto
University, Department of Pharmacology; Yoshida-Komoe, Sakyo-Ku,
Kyoto, Kyoto 606, Japan (Tel:81-75-753-4392, Fax:81-75-753-4693)

FEATURES

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/strain="129Sv"
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/number=1

ORIGIN

Query Match 46.5%; Score 544.8; DB 10; Length 895;
Best Local Similarity 78.2%; Pred. No. 6.9e-94;
Matches 654; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 12 GTTTCACCGCTGCAGAACCACTCTGTGAAAAAGGCACTCGCGGTGATGGCGG 71
Db 45 GTCTATCGCTGTCAAGACATCCACTGGGTGAAAGGGGCTCTCGCGCAAGATGGCGG 104
Qy 72 GGTGCTCTTACAGACCGGCTCTGTGGCACTGTGCGTGGGCTGTGCGCGCTC 131
Db 105 TGTGCTCTTACAGACCGGCTCTGTGGCACTGTGCGTGGGCTGTGCGCGCTC 164
Qy 132 GGGGCTGGGGTGGTGTGCGGGGTCCACTGCGCGCGCTCGCTCTTCAATGCT 191
Db 165 GGAAGCTGGGGTGGTGTGCGGGGTCCACTGCGCGCGCTCGCTCTTCAATGCT 224
Qy 192 GGTGTGTGCTGACCGGTCAACCACTGTGCGCAAGTGCCTCAAGCCGGTGTGCT 251
Db 225 CGTGTGTGCTTACCGGTCAACCACTGTGCGCAAGTGTCTATGATGCT 284
Qy 252 GGTGTGTGCTGACCGGTCAACCACTGTGCGCAAGTGTCTTGAACAATGCT 311
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Qy 312 GTGCCAAGCTTGTGCTTCAATGCTTGTGCGTCTCTGCACTGCAATGCT 371
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Qy 372 GGCATGGAAGTGTGCTTGTGCGTCTCTGCACTGCAATGCT 431

Db 405 GGTATATGGGGTGAAGTGTGCTGTCTGTGGACACCCCTTCTTACCAAGGACGT 464
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Db 525 TGGGCTCCCTTGTGCTTGTGGGAAGTTCGTGCACTGCCCCGCACTGTGCTT 584
Qy 552 TATTCAGATGTTCACAGAGAGGCTGCTGTGCTGGGTACTGTGTCTATCTC 611
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Qy 672 CCTTATGCGATGCAACCGGCTGAGCGGCAACCGGCTCTCTGCAACAGGAGCTGTGC 731
Db 705 CCTTATGCAATGCAACAGGCGCAGAGGCACTATCTCAACCGGCTCTCAAGGAGCGCG 764
Qy 732 CGAGCCGCGCGGAGACGGAAGGAGACCTCCCTCAACCGGCTGAGAGCTGATCACT 791
Db 765 CGAGTCAAGCTCAAGACTAAGGCAACGAGCGGCTCCCTGCACTCTTGGAGAGCTGACCACT 824
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RESULT 14

AC095991.3
WPCOMMENT
Sequence split into 4 fragments LOCUS AC095991 Accession AC095991
Fragment Name Begin End
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AC095991.1 100001 210000
AC095991.2 200001 310000
AC095991.3 300001 367632
Continuation (4 of 4) of AC095991 from base 300001 (AC095991 Rattus norvegicus clone CH2;

Query Match 46.3%; Score 541.6; DB 2; Length 67632;
Best Local Similarity 78.0%; Pred. No. 2.3e-93;
Matches 652; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
Qy 12 GTTTCACCGCTGCAGAACCACTCTGTGAAAAAGGCACTCGCGGTGATGGCGG 71
Db 63144 GTCTATCGCTGTCAAGACATCCACTGGGTGAAAGGGGCTCTCGCGCAAGATGGCGG 63203
Qy 72 GGTGCTCTTACAGACCGGCTCTGTGGCACTGTGCGTGGGCTGTGCGCGCTC 131
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Qy 132 GGGGCTGGGGTGGTGTGCGGGGTCCACTGCGCGCGCTCGCTCTTCAATGCT 191
Db 63264 CCGGCTGGGGTGGTGTGCGGGGTCCACTGCGCGCGCTCGCTCTTCAATGCT 63323
Qy 192 GGTGTGTGCTGACCGGTCAACCACTGTGCGCAAGTGCCTCAAGCCGGTGTGCT 251
Db 63324 AGTGTGTGCTGACCGGTCAACCACTGTGCGCAAGTGTCTATGATGCT 63383
Qy 252 GGTGTGTGCTGACCGGTCAACCACTGTGCGCAAGTGTCTTGAACAATGCT 311
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Db 63504 GGTATGGAAGTGTGCTTGTGCGTCTCTGCACTGCAATGCT 63563

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QY 612 CAGCCTCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671	
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QY 672 CCTGTATGCGATGCAACCGCGGCTGCAAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCT 731	
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RESULT 15

AC112324_0/c

WPCOMMENT

Sequence split into 4 fragments LOCUS AC112324 Accession AC112324

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AC112324_1 100001 210000

AC112324_2 200001 310000

AC112324_3 300001 357027

LOCUS AC112324 357027 bp DNA linear HTG 26-SEP-2002

DEFINITION Rattus norvegicus clone CH230-75L12, *** SEQUENCING IN PROGRESS

*** 11 unordered pieces.

AC112324 GI:23321735

HTG: HTGS PHASE1: HTGS DEAF1: HTGS ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 357027)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,

Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Burch, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Decker, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregergs, E., Geer, K., Gilly, R., Grady, M., Guerra, M., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Hayak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M.,

Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Kling, L., Kovar, C.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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TITLE

JOURNAL

Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshew, L., Louie, H., Lozano, R. J., Lu, X., Ma, D.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenan, E.,
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Plopper, F., Ponder, A., Popovic, D., Primm, E., Pu, L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reish, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorrell, R., Sosa, D.,
Steinle, M., Strong, N., Sutton, A., Svatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, T., Yoon, L., Yoon, V.,
Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 357027)

Worley, K. C.

Direct Submission

Submitted (21-FEB-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 357027)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (26-SEP-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Sep 26, 2002 this sequence version replaced gi:11737250.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the

sequence may extend beyond the ends of the clone and there may be

contigs that consist entirely of whole genome shotgun sequence

reads. Both end sequences and whole genome shotgun sequence only

contigs will be indicated in the feature table.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: G00G

Center clone name: CH230-75L12

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 294995 bases at least Q40

Consensus quality: 299994 bases at least Q30

Consensus quality: 302651 bases at least Q20

Estimated insert size: 390689; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draht_data.html)

NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently

consists of 11 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 7987: contig of 7987 bp in length
* 7988 8087: gap of unknown length
* 8088 15583: contig of 7496 bp in length
* 15584 15683: gap of unknown length
* 15684 133212: contig of 117529 bp in length
* 133213 133312: gap of unknown length
* 133313 261674: contig of 128362 bp in length
* 261675 261774: gap of unknown length
* 261775 274519: contig of 12745 bp in length
* 274520 285073: contig of 10454 bp in length
* 285074 285173: gap of unknown length
* 285174 327268: contig of 41995 bp in length
* 327269 331337: gap of unknown length
* 331338 331437: gap of unknown length
* 331438 344641: contig of 13204 bp in length
* 344642 351023: gap of unknown length
* 351024 351123: gap of 6282 bp in length
* 351124 357027: contig of 5904 bp in length.

FEATURES

source

1. 357027
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-75L12"

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/note="wgs contig"
5697..7987
misc_feature
/note="wgs contig"
8088..10145
misc_feature
/note="wgs contig"
10196..15583
misc_feature
/note="wgs contig"
261775..263469
misc_feature
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263520..269146
misc_feature
/note="wgs contig"
273264..274519
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274620..279177
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327269..329628
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/note="wgs contig"
329860..331337
misc_feature
/note="wgs contig"
333452..334831
misc_feature
/note="wgs contig"
342450..344641
misc_feature
/note="wgs contig"

ORIGIN

Query Match 46.3%; Score 541.6; DB 2; Length 110000;
Best Local Similarity 78.0%; Pred. No. 2.2e-93;
Matches 652; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

Qy 12 GTTTCACGCGTGCACAAACACCACTCTGTGAAAAAGCAACTCGCGGTGATGCGCGG 71
Db 108350 GTTCCTATCCGCTGCAGACGACCACTGGGTGGAACGGGCTCTCAAGCAACATGGGTG 108291
Qy 72 GGTGCTCTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGGGCTGCGCGGCTC 131
Db 108290 TGTGCTCTTCAGTGCAGACTGTGTGGCAACTCTCTGCGCTGTGTGCTGCGCGGATC 108231
Qy 132 GGGGCTGGGGTGTGTGTCTCGCGGCTCACTGCGCGCGCTGCGCTCTTACATGCT 191
Db 108230 CGGGCTGGGGTGTGTGTCTCGCGGCTCACTGCGCGCGCTGCGCTCTTACATGCT 108171

Qy 192 GGTGTGCGCTGACAGGTACACGACTTGTGGCAAGTGCCTCTAAGCCCGGTGTGCT 251
Db 108170 AGTGTGCGCTTACAGTACACGACTTGTGGCAAGTGTCTATACAGCCCATGTGCT 108111
Qy 252 GGTGCTTACGCTCAGAACCGAGTGTGCGGCTGTGCGCGCGCATTTGACAACTGCTT 311
Db 108110 GGTGCTTACGCGCAAAATCGAGCTTAAGGAACTGTGCGCTGTGCGCGCAACGATT 108051
Qy 312 GTGCCAAGCTTGTGCTTCTATGTCTCTTGTGGGCTCTCTGTGACACTGAACTGCT 371
Db 108050 ATGTGAAGCTTGTGCTTCTGTATGTCTTCTTGTGGGCTTGTGACCTTACAGCTACT 107991
Qy 372 GGCATGGAAGTGTGCTGCTCTCCCTAAGGACCTTCTTCTTACGAGGACAT 431
Db 107990 GGTATGGAAGTGTGCTGCTCTCTGCTGTGCTGTGCAACAGTGTGCGGCTTCTTGTGCTTCTG 107871
Qy 432 CACCTGCGCTGTGGGCACTGTGTGCGCCCGGTGTGAGCGCTTCTCTGCTTCTG 491
Db 107930 CACCGCGCGCGGAGTGTGCTGTGCAACAGTGTGCGGCGCTTCTTGTGCTTCTG 107871
Qy 492 CGGCTACCTTTCATAGGCTTGTGGGAATTTGTGCACTGTGCGCGGACCTGTGCTT 551
Db 107870 TGGCTCCCTTGTGCTGTGGGAATTTGTGCACTGTGCGGCTGCTTGTGCTT 107811
Qy 552 TATCAGATGTTCACAGAGAGGCTCGCTGTGCTGTGGGTACTGTGCTACTC 611
Db 107810 CATTCAGATGTTCACAGAGAGGCTCATTTCTGTGTAATAGCTTCTGTGCTACTC 107751
Qy 612 CAGCTCATGTGCGCTGTGTCTGTGCAACGCTGTGCAACCTTGTGCGGCAATGCGCA 671
Db 107750 CAGCTCATGTGCGCTGTGTCTGTGCAACGCTGTGCAACCTTGTGCGGCAATGCGCA 107691
Qy 672 CCTTATGTGATGACACCGGCTGTGAGGAGGACCGGCTCTGTGACCAAGGACTGTG 731
Db 107690 CCTTATGTGATGACACCGGCTGTGAGGAGGACCAATCCCGCTGTGCAAGGAGCGCG 107631
Qy 732 CGAGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 791
Db 107630 CAGTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 107571
Qy 792 CTTGCTGTGCGCTGTGATGACGCTGTCTTCACTATGTGTCTGTGCGCGTAATG 847
Db 107570 TGTGCTGTGCGCTGTGATGACGCTGTCTTCACTATGTGTCTGTGCGCGTAATG 107515

Search completed: April 22, 2005, 15:32:10
Job time : 5338.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 09:24:18 ; Search time 707.49 Seconds
(Without alignments)
9798.042 Million cell updates/sec

Title: US-10-689-861-1
Perfect score: 1171
Sequence: 1 atgaagtcgcgcgtctaccg.....acatgcatccagtcgtga 1171

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

1: geneseqn1980s:*\n2: geneseqn190s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2004as:*\n12: geneseqn2004bs:*\n13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	992.8	84.8	1505	10	AD607082
2	979	83.6	1253	4	ABA09244
3	979	83.6	1253	4	AAK53126
4	979	83.6	1253	10	AD608862
5	979	83.6	1303	4	AAK52142
6	979	83.6	1488	2	AAT37402
7	976	83.3	1077	12	AD030026
8	950.6	81.2	1264	3	AAA27056
9	848.4	72.5	14607	3	AAA35113
10	848.4	72.5	14607	3	AAFP21235
11	848.4	72.5	14607	10	ABZ96929
12	848.4	72.5	14607	11	ABD20778
13	847	72.3	1216	3	AAA35105
14	847	72.3	1216	3	AAFP21227
15	847	72.3	1216	10	ABZ96921
16	847	72.3	1216	10	ACA56876
17	847	72.3	1216	11	ABD20770
18	847	72.3	1216	12	AD156672
19	830	70.9	964	12	ACH90941
20	590	50.4	597	12	ACH76886

21	556	47.5	1074	12	AD030316	Ad030316 Mouse GPC
22	556	47.5	1315	10	ADB58427	AdB58427 Toxicity-
23	554.4	47.3	1240	2	AAT05172	Aat05172 Prostagla
24	552.8	47.2	1071	2	AAT05171	Aat05171 Prostagla
25	371	31.7	371	12	ACH90586	ACH90586 Human gen
26	335	28.6	495	3	AAA35104	AAA35104 Human ade
27	335	28.6	495	3	AAFP21226	Aaf21226 Human low
28	335	28.6	495	8	ABZ42748	Abz42748 Human pro
29	335	28.6	495	10	ABZ96920	Abz96920 Human nuc
30	335	28.6	495	11	ABD20769	Abd20769 Human pul
31	335	28.6	495	13	ADP55148	Adp55148 Human PRO
32	211	18.0	1077	3	AAA34921	Aaa34921 Human ade
33	211	18.0	1077	3	AAFP21043	Aaf21043 Human low
34	211	18.0	1077	11	ABZ96737	Abz96737 Human nuc
35	211	18.0	1077	11	ABD20586	Abd20586 Human pul
36	211	18.0	2296	2	AAV12457	Aav12457 Human HP4
37	211	18.0	2296	6	ABK88459	Abk88459 Human CDN
38	211	18.0	2395	12	AD005737	Ad005737 Human pro
39	211	18.0	9060	3	AAA34925	Aaa34925 Human pro
40	211	18.0	9060	3	AAFP21047	Aaf21047 Human low
41	211	18.0	9060	10	ABZ96741	Abz96741 Human nuc
42	211	18.0	9060	11	ABD20590	Abd20590 Human pul
43	210.2	18.0	36509	13	ACH37241	ACH37241 Human per
44	209.4	17.9	1077	12	AD030028	Ad030028 Human GPC
45	209.4	17.9	2372	3	AAA34919	Aaa34919 Human ade

ALIGNMENTS

RESULT 1	
AD607082	AD607082 standard; DNA; 1505 BP.
XX	
XX	AD607082;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Novel coding sequence (useful for identifying genetic disorders) #148.
XX	
KW	novel gene; novel protein; tissue marker; molecular weight marker;
KW	chromosome marker; genetic disorder; gene; db.
XX	
OS	Unidentified.
XX	
PN	MO2003054152-A2.
XX	
PD	03-JUL-2003.
XX	
XX	
PF	10-DEC-2002; 2002W0-US039555.
XX	
PR	10-DEC-2001; 2001US-0339739P.
PR	11-DEC-2001; 2001US-0339453P.
PR	14-MAR-2002; 2002US-0365091P.
PR	14-MAR-2002; 2002US-0365384P.
PR	12-APR-2002; 2002US-0372381P.
PR	12-APR-2002; 2002US-0372615P.
PR	22-APR-2002; 2002US-00128558.
PR	24-APR-2002; 2002US-0376045P.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Qa, Wang J;
PI	Ghosh M, Xue AJ, Weinman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI	Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX	
DR	WPI; 2003-569235/53.
XX	
PT	P-PSDB; AD607993.
XX	
PT	New polynucleotides, useful for expressing recombinant proteins for
PT	analysis, characterization or therapeutic use, or as markers for tissues
PT	in which the corresponding protein is preferentially expressed.
XX	

PS Claim 1; SEQ ID NO 148; 1177bp; English.

XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present DNA sequence represents a gene of the
CC invention.

XX Sequence 1505 BP; 265 A; 434 C; 441 G; 365 T; 0 U; 0 Other;

Query Match 84.8%; Score 992.8; DB 10; Length 1505;
Best Local Similarity 92.3%; Pred. No. 1.1e-225;
Matches 1069; Conservative 0; Mismatches 57; Indels 32; Gaps 1;

QY 1 ATGAAGTCGCGGTTTCAACCGCTGCAGAACACCACTCTGTGAAAAAGCAACTGAGCG 60
DB 231 ATGAAGTCGCGGTTTCAACCGCTGCAGAACACCACTCTGTGAAAAAGCAACTGAGCG 290
QY 61 GATGATGGGCGGGGATGCTTCAAGACCGGCTCTGTGGCAACCTGTGCGGCTGAGGCTG 120
DB 291 GATGATGGGCGGGGATGCTTCAAGACCGGCTCTGTGGCAACCTGTGCGGCTGAGGCTG 350
QY 121 CTGGCCGCTCGGGGCTGGGGGATGCTCGCGGCTTCACCTGCGCCGCTGCGCTG 180
DB 351 CTGGCCGCTCGGGGCTGGGGGATGCTCGCGGCTTCACCTGCGCCGCTGCGCTG 410
QY 181 TTCTACATGCTGTGTGTGGCTGAGCGGTCAACGACTTGTGGGCAAGTGTCTTAC 240
DB 411 TTCTACATGCTGTGTGTGGCTGAGCGGTCAACGACTTGTGGGCAAGTGTCTTAC 470
QY 241 CCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 471 CCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
QY 301 GACAACTGCTGTGTGCAAGGCTTTCGCTTTCATGCTCTTCTTGGGCTCTCTGACA 360
DB 531 GACAACTGCTGTGTGCAAGGCTTTCGCTTTCATGCTCTTCTTGGGCTCTCTGACA 590
QY 361 CTGCAACTCTGTGGCAATGCACTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTAC 420
DB 591 CTGCAACTCTGTGGCAATGCACTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTAC 650
QY 421 CGAGCGCACTACCTGCGGCTGGGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 651 CGAGCGCACTACCTGCGGCTGGGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
QY 481 CTGGCTTTCTGCGGCTACCTTTCATGAGGCTTCGAGAAATTGCTGACATCTGCCCGGC 540
DB 711 CTGGCTTTCTGCGGCTACCTTTCATGAGGCTTCGAGAAATTGCTGACATCTGCCCGGC 770
QY 541 ACTGTGTCTTTATTCAGATGCTTCACAGAGAGGCTCTGTGCTGCTGCTGCTGCT 600
DB 771 ACTGTGTCTTTATTCAGATGCTTCACAGAGAGGCTCTGTGCTGCTGCTGCTGCT 830
QY 601 GTGCTCTACTCCAGGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 831 GTGCTCTACTCCAGGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
QY 661 GCCATGCGCAACCTCTATGAGATGCACTGCGGCTGAGGAGGACCCGCTCTGACCC 720
DB 891 GCCATGCGCAACCTCTATGAGATGCACTGCGGCTGAGGAGGACCCGCTCTGACCC 950
QY 721 AGGGAATGTGCGAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 951 AGGGAATGTGCGAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
QY 781 CTGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 1011 CTGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070

QY 841 GTAATG-----CATTGTTCTGAGTCCCG 868
DB 1071 GTAATGAGTCCCGGCGCCCGAGCAGAGGCACTGATCTGCGGCGCGAGT 1130
QY 869 CCAAGCACCTGGAGTATGAGCTTGAAGAAACATTTTACGTCTCTCTCTT 928
DB 1131 CCGGGGGGAGAGGTGAGCGGATGCGGATGACGCGCGCGAGCGAGCTGCGCTGG 1190
QY 929 TCTCCCAAGTATCGCCTTACTATGAGAGCATTTAAGATGTCAAGAGAAAAACAGAAC 988
DB 1191 GCCAGAGATATGCGCCTTACTATGAGAGCATTTAAGATGTCAAGAGAAAAACAGAAC 1250
QY 989 TCTGAAGAGCAGAGACCTCCGAGCTTCGATTTCTATCTGTATTTCAATTGTCAGC 1048
DB 1251 TCTGAAGAGCAGAGACCTCCGAGCTTCGATTTCTATCTGTATTTCAATTGTCAGC 1310
QY 1049 CCTTGATTTTATATCAATTTTCAATGATCTGATTTTCAAGATTTTC 1108
DB 1311 CCTTGATTTTATATCAATTTTCAAGATCTCAAGATTTTCAAGATTTTC 1370
QY 1109 ATTAGACTCTTAGGTAC 1126
DB 1371 ATTAGACTCTTAGGTAC 1388

RESULT 2

ABA09244
ID ABA09244 standard; cDNA; 1253 BP.

XX ABA09244;

DT 11-JAN-2002 (first entry)

XX Human prostaglandin DP receptor homologue cDNA, SEQ ID NO:1020.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhiblin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antistatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytoskeletal; osteopathic; vasotropic; cardiac; virucide; antibacterial;
KW antifungal; vulnery; antidiarr; ss.

XX Homo sapiens.

OS WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457740/49.

XX P-Psdb; ABB12000.

XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.

PS Claim 1; Page 860-861; 1963pp; English.

PF 05-FEB-2001; 2001MO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejman T, Goodrich R;
 DR WPI, 2001-476283/51.
 DR P-SDB; AAM79993.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PS Claim 1; Page 4907; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX
 SQ Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
 Query Match 83.6%; Score 979; DB 4; Length 1253;
 Best Local Similarity 92.2%; Pred. No. 2e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;
 QY 1 ATGAAGTCGCGGTTCTACCGCTGCGCAGAACCACTCTGGGAAAAGGCACTGGCG 60
 DB 122 ATGAAGTCGCGGTTCTACCGCTGCGCAGAACCACTCTGGGAAAAGGCACTGGCG 181
 QY 61 GTGATGGGCGGGGTCCTTACAGACCGGCTCTGGGCAACCTGCTGGGCTG 120
 DB 182 GTGATGGGCGGGGTCCTTACAGACCGGCTCTGGGCAACCTGCTGGGCTG 241
 QY 121 CTGGCGGCTGGGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 180
 DB 242 CTGGCGGCTGGGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 301
 QY 181 TTCTACATGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
 DB 302 TTCTACATGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 361
 QY 241 CCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 300
 DB 362 CCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 421
 QY 301 GAAACCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
 DB 422 GAAACCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 481
 QY 361 CTGCAACTCTGGGCAATGGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 420
 DB 482 CTGCAACTCTGGGCAATGGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 541

QY 421 CGAGGCAATCAACCTGCGGCTGGGCGCATGTGTGTGCCCCGGGTGTGAGCCCTTCTCC 480
 DB 542 CGAGGCAATCAACCTGCGGCTGGGCGCATGTGTGTGCCCCGGGTGTGAGCCCTTCTCC 601
 QY 481 CTGGCTTCTGGGCGGCTGACCTTTCAATGGGCTTGGGAAATTTGGTGTGACTGCCCCGGC 540
 DB 602 CTGGCTTCTGGGCGGCTGACCTTTCAATGGGCTTGGGAAATTTGGTGTGACTGCCCCGGC 661
 QY 541 ACCTGTGCTTTATTCAGATGTGCAAGAGAGGCTGCTGTGGTGTGGGCTGACTCT 600
 DB 662 ACCTGTGCTTTATTCAGATGTGCAAGAGAGGCTGCTGTGGTGTGGGCTGACTCT 721
 QY 601 GTGTCTTACTCCAGCTTCAATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 DB 722 GTGTCTTACTCCAGCTTCAATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 781
 QY 661 GCCATGCGAACCCTATGAGATGCAACGGGCGGCTGCAAGGCAACCGGCTGCTGACCC 720
 DB 782 GCCATGCGAACCCTATGAGATGCAACGGGCGGCTGCAAGGCAACCGGCTGCTGACCC 841
 QY 721 AGGATCTGTGCGAGCGCGCGCGAGAGGAGGAGCTGCTGAGCCCTGAGAGAG 780
 DB 842 AGGATCTGTGCGAGCGCGCGCGAGAGGAGGAGCTGCTGAGCCCTGAGAGAG 901
 QY 781 CTGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 902 CTGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 QY 841 GTAATTGCAATTTGTTCTGTGAGTCCCCCGCAAGACCTGGGAGTGTGAGGCTTGAAG 900
 DB 962 GTAATT----- 967
 QY 901 AAACATTTTCAGTGTGCT 960
 DB 968 -----TATCGGCTTACTATGAGCAATT 990
 QY 961 TAAAGATGTCAAG 1020
 DB 991 TAAAGATGTCAAG 1050
 QY 1021 ATTCTATCTGTGATTTCAATTGTGAGAGCTTGAATTTTATCATTTTATCATTTTCAAT 1080
 DB 1051 ATTCTATCTGTGATTTCAATTGTGAGAGCTTGAATTTTATCATTTTATCATTTTCAAT 1110
 QY 1081 ATTTCCGATATTTTTCACAGATTTTTCATTTAGACTCTTATGATACAGAGAGCGGTGAG 1140
 DB 1111 ATTTCCGATATTTTTCACAGATTTTTCATTTAGACTCTTATGATACAGAGAGCGGTGAG 1170
 QY 1141 CAATTCACCTAACATGGAATTCAGTGTGGA 1171
 DB 1171 CAATTCACCTAACATGGAATTCAGTGTGGA 1201
 RESULT 4
 ADE08862
 ID ADE08862 standard; DNA; 1253 BP.
 XX
 AC ADE08862;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 XX Novel DNA-related contig nucleotide sequence #106.
 XX
 XX novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; contig; ds.
 OS Unidentified.
 XX
 PN W02003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002MO-US039555.

XX 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Weinman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
 XX WPI; 2003-569235/53.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Disclosure, SEQ ID NO 1928; 1177bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present DNA sequence was used in the
 CC exemplification of the invention.
 XX
 SO Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
 Query Match 83.6%; Score 979; DB 10; Length 1253;
 Best Local Similarity 92.2%; Pred. No. 2e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

DB 602 CTGGCTTTCTGCGCGCTACCTTTTCATGGGCTTGGGAAAGTTGTCGACGATCTGCCCCG 661
 QY 541 ACCGTGCTTTATATCCAGATGATCCAGAGAGAGGCTGCTGTGCTGGGTAATCTT 600
 DB 662 ACCGTGCTTTATATCCAGATGATCCAGAGAGAGGCTGCTGTGCTGGGTAATCTT 721
 QY 601 GTGCTTACTCCAGCCTCATGGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660
 DB 722 GTGCTTACTCCAGCCTCATGGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 781
 QY 661 GCCATGCGCAACTCTATGATGATGACCGGCGCTGACAGGCGCCCTCTGTGACC 720
 DB 782 GCCATGCGCAACTCTATGATGATGACCGGCGCTGACAGGCGCCCTCTGTGACC 841
 QY 721 AGGAGCTGTGCGAGCGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 842 AGGAGCTGTGCGAGCGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 901
 QY 781 CTGATCACCCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 840
 DB 902 CTGATCACCCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 961
 QY 841 GTATTGCAATTTCTTCTGTGAGATCCCGGCAAGACACTGGAGTATGAGGCTTGAGG 900
 DB 962 GTAAAT----- 967
 QY 901 AATCATTTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 960
 DB 968 -----TATGCGGCTTACTATGAGCATT 990
 QY 961 TAAGATGTCAG 1020
 DB 991 TAAGATGTCAG 1050
 QY 1021 ATTCTATCTGTGATTTCAATGTGACACCTTGATTTTATATTTGATCTCCAGT 1080
 DB 1051 ATTCTATCTGTGATTTCAATGTGACACCTTGATTTTATATTTGATCTCCAGT 1110
 QY 1081 ATTGGATATTTTTCACAGATTTTCATTAACCTTAGGTACAGAGCGGCTGACG 1140
 DB 1111 ATTGGATATTTTTCACAGATTTTCATTAACCTTAGGTACAGAGCGGCTGACG 1170
 QY 1141 CAATTCACATCAATGAAATTCAGTGTGA 1171
 DB 1171 CAATTCACATCAATGAAATTCAGTGTGA 1201

RESULT 5
 AAK52142
 ID AAK52142 standard; cDNA; 1303 BP.
 XX
 AC AAK52142;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 687.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 XX
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEO INC.

PI Tang YT, Liu C, Dirmnac RT, Aundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejrtman T, Goodrich R;

XX WPI; 2001-476283/51.
 XX P-PSDB; AAM79009.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.

XX Claim 1; Page.2387-2388; 6221p; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 1303 BP; 198 A; 426 C; 372 G; 307 T; 0 U; 0 Other;

Query Match 83.6%; Score 979; DB 4; Length 1303;
 Best Local Similarity 92.2%; Pred. No. 2e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAGTGGCGGCTTTCACCGCTGCCAGAACCACTCTGTGAAAAAGCACTGGCG 60
 DB 166 ATGAGTGGCGGCTTTCACCGCTGCCAGAACCACTCTGTGAAAAAGCACTGGCG 225
 QY 61 GTGATGGGCGGGGNGCTCTTCAGACCGGCTCCTGGGCAACCTGTGGCTGGGGCTG 120
 DB 226 GTATGGGCGGGGNGCTCTTCAGACCGGCTCCTGGGCAACCTGTGGCTGGGGCTG 285
 QY 121 CTGGCGGCTCGGGGCTGGGGGTGTGTCTGGCGGTCTCACTGGCGCCGCTCGGTG 180
 DB 286 CTGGCGGCTCGGGGCTGGGGGTGTGTCTGGCGGTCTCACTGGCGCCGCTCGGTG 345
 QY 181 TTCTACATGT 240
 DB 346 TTCTACATGT 405
 QY 241 CCGGT 300
 DB 406 CCGGT 465
 QY 301 GACAACTCGTTGTGCCAAGCTTTCGCTTTCATGTCTTCTTTTGGGCTCTCTTGACA 360
 DB 466 GACAACTCGTTGTGCCAAGCTTTCGCTTTCATGTCTTCTTTTGGGCTCTCTTGACA 525
 QY 361 CTGCAACTCTGTGGCATGAGCACTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 526 CTGCAACTCTGTGGCATGAGCACTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
 QY 421 CGACGGCAGATCACTCGGCTGTGGGCGCACTGGTGGCCCGGGGTGTGAGCGCTTCTCC 480
 DB 586 CGACGGCAGATCACTCGGCTGTGGGCGCACTGGTGGCCCGGGGTGTGAGCGCTTCTCC 645
 QY 481 CTGGCTTTCGTGGCGCTACCTTTCATGGGCTTTCGGGAAGTTCTGTGAGTACTGCCCGGC 540

DB 646 CTGGCTTTCGTGGCGCTACCTTTCATGAGGCTTTCGGGAAGTTCTGTGAGTACTGCCCGGC 705
 QY 541 AACTGTGTCTTATATCAGATGATGCAAGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGT 600
 DB 706 AACTGTGTCTTATATCAGATGATGCAAGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGT 765
 QY 601 GTGTCTTACTCCAGCTCATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 DB 766 GTGTCTTACTCCAGCTCATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 825
 QY 661 GCGATCGCAACTCTTATGCGATGCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 DB 826 GCGATCGCAACTCTTATGCGATGCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 885
 QY 721 AGGACGTGTGGCGAGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 DB 886 AGGACGTGTGGCGAGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
 QY 781 CTGATCACTCTCTGT 840
 DB 946 CTGATCACTCTCTGT 1005
 QY 841 GTTATTCATTTTCTTGTGAGTCCCGGCAAGACCTGGAGTGTGAGGCTTGAAG 900
 DB 1006 GTTATTT----- 1011
 QY 901 AATCATTTACAGTGTGTCT 960
 DB 1012 -----TATCGGCTTACTATGAGACATT 1034
 QY 961 TAAGATGTCAAGAGAAAAAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 1035 TAAGATGTCAAGAGAAAAAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1094
 QY 1021 ATTTTATCTGTGATTTTCAATTTGTGAGACCTTGTGATTTTATCATTTTGTGAGTCTGAGT 1080
 DB 1095 ATTTTATCTGTGATTTTCAATTTGTGAGACCTTGTGATTTTATCATTTTGTGAGTCTGAGT 1154
 QY 1081 ATTTGATATTTTTCACAGATTTTCAATTTGTGAGACCTTGTGATTTTATCATTTTGTGAGTCTGAGT 1140
 DB 1155 ATTTGATATTTTTCACAGATTTTCAATTTGTGAGACCTTGTGATTTTATCATTTTGTGAGTCTGAGT 1214
 QY 1141 CAATTCACCTAAAGAGAAATCCAGTCTGTGA 1171
 DB 1215 CAATTCACCTAAAGAGAAATCCAGTCTGTGA 1245

RESULT 6
 AAT37402
 ID AAT37402 standard; DNA; 1488 BP.
 XX
 AC AAT37402;
 DT 11-MAR-1997 (first entry)
 XX
 DE Prostaglandin DP receptor coding sequence.
 XX
 KW Prostaglandin DP receptor; human; prostanoil receptor; blood platelet;
 KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
 KW mouse; prostaglandin-related disease; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 349..1429
 FT /tag= a
 FT /product= "prostaglandin DP receptor"
 PN W09623066-A2.
 XX
 PD 01-AUG-1996.
 XX

PF 23-JAN-1996; 96WO-CA000047.
 XX 26-JAN-1995; 95US-00378682.
 XX (MERI) MERCK FROSST CANADA INC.
 XX Abramowitz M, Bole Y, Welters K, Sawyer N, Slietzel DM;
 PI WPI; 1996-362690/36.
 DR P-RSDB; AAW03516.
 XX
 PT Human prostaglandin DP receptor and related DNA - used to identify
 PT Receptor modulators to treat prostaglandin-related diseases.
 XX
 PS Claim 4; Page 41-42; 49pp; English.

CC This sequence represents the coding sequence for the human prostaglandin
 CC DP receptor. The DP receptor is the least ubiquitous and least abundant
 CC of the prostanoicid receptors. The DP receptors are thought to be
 CC distributed mainly in blood platelets, smooth muscle of various tissues,
 CC and nervous tissue (including the central nervous system). However, many
 CC of the actions and distribution of the DP receptor is species dependent.
 CC The encoded DP receptor is a G protein-coupled receptor which can
 CC specifically bind prostaglandin molecules. This sequence was isolated
 CC using primers (see AAT37403 and AAT37404) based on the N-terminal
 CC sequence, and an internal sequence from purified mouse DP. The human
 CC prostaglandin DP receptor can be used to identify modulators of the
 CC receptor. The identified modulators can then be used to treat
 CC prostaglandin-related diseases, and for modulating the effects of
 CC prostaglandins on the DP receptor

Sequence 1488 BP; 232 A; 482 C; 423 G; 351 T; 0 U; 0 Other;

Query Match 83.6%; Score 979; DB 2; Length 1488;
 Best Local Similarity 92.2%; Pred. No. 2,1e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCGCGCTTACCGCTGCAAGACCACTCTGTGAAAAAGGCACTCGGCG 60
 DB 350 ATGAAGTCGCGCTTACCGCTGCAAGACCACTCTGTGAAAAAGGCACTCGGCG 409
 QY 61 GTGATGAGGCGGAGTGTCTTACAGACCGGCTCTGTGCAACTGTGCTGCGGCTG 120
 DB 410 GTGATGAGGCGGAGTGTCTTACAGACCGGCTCTGTGCAACTGTGCTGCGGCTG 469
 QY 121 CTGGCGCGCTCGGCGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 180
 DB 470 CTGGCGCGCTCGGCGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 529
 QY 181 TTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 530 TTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
 QY 241 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 590 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
 QY 301 GACAATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 650 GACAATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
 QY 361 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 710 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
 QY 421 CGACGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 770 CGACGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
 QY 481 CTGGCTTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 830 CTGGCTTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889

QY 541 ACCTGCTGCTTTATTCAGATGATGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCT 600
 DB 890 ACCTGCTGCTTTATTCAGATGATGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCT 949
 QY 601 GTGCTTACTTCCAGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 950 GTGCTTACTTCCAGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
 QY 661 GCCATGGGCAACCTTATGAGGATGCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 1010 GCCATGGGCAACCTTATGAGGATGCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
 QY 721 AGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 1070 AGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129
 QY 781 CTGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 1130 CTGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
 QY 841 GTTATTGCAATTGTCTCTGAGATCCCGGCAAGACCTGAGATGAGGCTTGGAG 900
 DB 1190 GTTATT-----
 QY 901 AAACATTTTCAAGTGTGCTGCT 960
 DB 1196 -----TATCGGCTTACTATGAGCATTT 1218
 QY 961 TAAAGATGTCAG 1020
 DB 1219 TAAAGATGTCAG 1278
 QY 1021 ATTTTATCTGATTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080-
 DB 1279 ATTTTATCTGATTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338
 QY 1081 ATTTTATCTGATTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 DB 1339 ATTTTATCTGATTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
 QY 1141 CAATTCACATTAACATGAATTCAGATCTGTGA 1171
 DB 1399 CAATTCACATTAACATGAATTCAGATCTGTGA 1429

RESULT 7
 ADO30026
 ID ADO30026 standard; cDNA; 1077 BP.
 XX
 AC ADO30026;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 XX Human GPCR PTGDR polynucleotide, SEQ ID NO:1128.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytostatic; antiinflammatory; vasotropic; antidiarrhetic; antidiabetic;
 KW CNS; central nervous system; respiratory; antidiarrhetic; antidiabetic;
 KW virostatic; hepatotropic; antibacterial; antianemic; antiseborrheic;
 KW dermatological; antihypertensive; antiallergic; anorectic;
 KW immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KW gene; ss.
 XX
 XX Homo sapiens.
 XX

XX MO2004040000-A2.
 XX 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 XX 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
 XX Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX WPI; 2004-390329/36.
 XX P-PSDB; ADO29614.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 XX compounds that modulates diagnosing and treating disease condition
 XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
 XX pectoris, Parkinson's disease.
 XX
 XX Claim 151; SEQ ID NO 1128; 542pp; English.
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 XX (GPCRs) and nucleic acids encoding them. The invention also relates to
 XX sequences at least 90% identical to the GPCR proteins and nucleic acids
 XX of the invention; methods of treating, preventing or diagnosing diseases
 XX associated with GPCRs of the invention; methods of screening for
 XX compounds useful in the treatment of GPCR-related diseases; a transgenic
 XX mouse comprising a GPCR gene of the invention; a mouse comprising a
 XX mutation in a GPCR transgene or in an endogenous GPCR gene, cells derived
 XX from the transgenic mice; kits comprising several mice, each of which has
 XX a mutation in a different GPCR gene of the invention; and kits comprising
 XX probes which hybridize to GPCR polynucleotides of the invention. The
 XX invention further discloses variants of the GPCR polypeptides and vectors
 XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 XX be used in the diagnosis, treatment or prevention of a wide variety of
 XX diseases including neurological disorders (e.g., Alzheimer's disease,
 XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 XX disorders of the adrenal gland; disorders of the colon or intestine
 XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 XX myocardial infarction); muscular disorders; blood disorders (e.g.,
 XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
 XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 XX nucleic acid of the invention. Note: The full sequence data for this
 XX patent did not form part of the printed specification; those sequences
 XX not shown were obtained in electronic format directly from WPIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 1077 BP; 169 A; 336 C; 310 G; 262 T; 0 U; 0 Other;
 XX
 XX Query Match 83.3%; Score 976; DB 12; Length 1077;
 XX Best Local Similarity 92.2%; Pred. No. 9, 8e-222;
 XX Matches 1077; Conservative 0; Mismatches 0; Indels 91; Gaps 1
 XX
 XX 1 ATGAAGTGGCGGCTTTACCGCTCCAGAACACCACTCTGTGGAAAAAGGCAACTCGGCG 60
 XX 1 ATGAAGTGGCGGCTTTACCGCTCCAGAACACCACTCTGTGGAAAAAGGCAACTCGGCG 60
 XX
 XX 61 GTGATGGGCGGGGCTCTTCACGACCGGCTCTCGGGCAACCTGTGGCCCTGGGGCTG 120
 XX 61 GTGATGGGCGGGGCTCTTCACGACCGGCTCTCGGGCAACCTGTGGCCCTGGGGCTG 120
 XX
 XX 121 CTGGGGCGGCTCGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCT 180
 XX 121 CTGGGGCGGCTCGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCT 180

[illegible]

XX AAA27056;
 AC 22-AUG-2000 (first entry)
 DT
 XX Human cell surface receptor protein cDNA sequence #13.
 DE
 XX Human; HCSR; cytosolic; antiarthritic; antineumatic; antiaesthetic;
 XX immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 XX neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
 XX rheumatoid arthritis; asthma; atherosclerosis; akathisia;
 XX Alzheimer's diseases; multiple sclerosis; epilepsy; ss.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 130..1239
 FT /*tag= a
 FT /product= "HCSR-13"
 PN MO200028032-A2.
 XX 18-MAY-2000.
 PD
 XX 12-NOV-1999; 99MO-05026742.
 PF
 XX 12-NOV-1998; 98US-00191280.
 PR 07-DEC-1998; 98US-00206647.
 PR 08-MAR-1999; 99US-0123404P.
 XX (INCY-) INCYTE PHARM INC.
 XX PA
 XX PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
 PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
 DR P-PSDB; AAY94346.
 XX MPI; 2000-376546/32.
 PT
 PT New human cell surface receptor protein and polynucleotide useful for
 PT diagnosis, prevention and treatment of cancer, immune disorders,
 PT infection and neuronal disorders.
 XX
 XX Claim 9; Page 97; 97p; English.
 PS
 XX The present sequence encodes a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-13. The nucleotide sequence was identified in
 CC Incyte Clone 3576503 from the cDNA library BRONOT01, which was made from
 CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
 CC to assemble the consensus sequence. BLAST analysis showed that the
 CC sequence is homologous to DR, prostanoic receptor 9940379. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HCSR may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR
 CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds
 XX
 SQ Sequence 1264 BP; 189 A; 404 C; 368 G; 303 T; 0 U; 0 Other;
 Query Match 81.2%; Score 950.6; DB 3; Length 1264;
 Best Local Similarity 91.7%; Pred. No. 1,1e-215;
 Matches 1076; Conservative 0; Mismatches 4; Indels 93; Gaps 3;
 QY 1 ATGAAGTCGCGGTTCTTACCGCTCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 60
 DB 130 ATGAAGTCGCGGTTCTTACCGCTCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 189

QY 61 GTGATGCGCGGGGCTCTTACAGCACCGGCTCTGGGCAACCTGTGCGCTGGGCTG 120
 DB 190 GTGATGCGCGGGGCTCTTACAGCACCGGCTCTGGGCAACCTGTGCGCTGGGCTG 249
 QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 DB 250 CTGGCGCGCTCGGGGCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 309
 QY 181 TTCTTACATGCTGT 240
 DB 310 TTCTTACATGCTGT 369
 QY 241 CCGGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 300
 DB 370 CCGGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 429
 QY 301 GACCACTGCTGT 360
 DB 430 GACCACTGCTGT 489
 QY 361 CTGCAACTCTGTGCGCATGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCA 420
 DB 490 CTGCAACTCTGTGCGCATGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCA 549
 QY 421 CGACGCGACATCACCTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGT 480
 DB 550 CGACGCGACATCACCTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGT 609
 QY 481 CTGCGCTTCTGTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 540
 DB 610 CTGCGCTTCTGTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 669
 QY 541 ACCTGTGCTTATTCAGATGTGTCAGATGTGTCAGATGTGTCAGATGTGTCAGATGTGTC 600
 DB 670 ACCTGTGCTTATTCAGATGTGTCAGATGTGTCAGATGTGTCAGATGTGTCAGATGTGTC 729
 QY 601 GTGCTTACCTCCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 660
 DB 730 GTGCTTACCTCCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 789
 QY 790 GCCATGCGCAACTCTATGTGATGCACTGCGGCTGCAAGGCGGCACTGCGGCTGCAAG 849
 DB 721 AGGACCTGTGCGGAGCG 780
 QY 850 AGGACCTGTGCGGAGCG 909
 DB 781 CTGATCACCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 840
 QY 910 CTGATCACCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 969
 DB 841 GTATTGCAATTTGTTCTGTGAGTCCCGCCGCAAGACCTGTGAGTGTGAGGCTTGAGG 900
 QY 970 GTATT----- 975
 DB 901 AAACATTTTACGTGCTGCT 960
 QY 976 -----TATCGGCTTACTATGAGCATTT 998
 DB 961 TAGGATGTCAAGGAGAAAAAG 1019
 QY 999 TAGGATGTCAAGGAGAAAAAG 1058
 DB 1020 GATTTCATCTGTGATTTTCAATTTGAGACCTTGTGATTTTATCATTTTATCATTTTCA 1079
 QY 1059 GATTTCATCTGTGATTTTCAATTTGAGACCTTGTGATTTTATCATTTTATCATTTTCA 1118
 DB 1080 TATTTCGATTTTATTTTCAAGAG-TTTTCAATTTGAGACCTTGTGATTTTATCATTTTCA 1138
 QY 1119 TATTTCGATTTTATTTTCAAGAG-TTTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1178

QY 1139 AGCAATTCACCTAATGAGTCACTGCTGGA 1171
 DB 1179 AGCAATTCACCTAATGAGTCACTGCTGGA 1211

RESULT 9
 ID AAA35113 standard; DNA; 14607 BP.
 XX AAA35113;
 AC
 XX
 XX 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2802.

XX Human adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiasthmatic; cytoskeletal; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; BS.

XX Homo sapiens.
 OS
 XX
 XX MO200009525-A2.
 XX 24-FEB-2000.
 XX 03-AUG-1999; 99MO-US017712.
 PF
 XX 03-AUG-1998; .98US-0095212P.
 PR
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 XX Nyce JM;
 PI
 XX
 XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 PT
 XX

PS Disclosure; Page 1064-1068; 1343bp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiasthmatic,
 CC antiasthmatic, cytoskeletal and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35112 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

SQ Sequence 14607 BP, 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;
 Query Match 72.5%; Score 848.4; DB 3; Length 14607;
 Best Local Similarity 94.4%; Pred. No. 5.1e-191;
 Matches 891; Conservative 0; Mismatches 51; Indels 2; Gaps 1;

QY 1 ATGAAGTCCCGCTTCTTACCGCTGCGCAAGAACCACTCTGTGGAAAAAGCAACTGGCG 60
 DB ATGAAGTCCCGCTTCTTACCGCTGCGCAAGAACCACTCTGTGGAAAAAGCAACTGGCG 904
 QY 61 GTGATGGGGGGGGGGTGTCTTTCAGCAACCGGCTCTGGGGCAACTGGTGGCGGGGGCTG 120
 DB GTGATGGGGGGGGGGTGTCTTTCAGCAACCGGCTCTGGGGCAACTGGTGGCGGGGGCTG 964
 QY 905 GTGATGGGGGGGGGGTGTCTTTCAGCAACCGGCTCTGGGGCAACTGGTGGCGGGGGCTG 964
 QY 121 CTGGCGCGCTCGGGGGCTGGGGGGTGTCTGCGCGCGCTGCACTGCGCGCGCGCTGCGCTG 180
 DB CTGGCGCGCTCGGGGGCTGGGGGGTGTCTGCGCGCGCTGCACTGCGCGCGCGCTGCGCTG 1024
 QY 965 CTGGCGCGCTCGGGGGCTGGGGGGTGTCTGCGCGCGCTGCACTGCGCGCGCGCTGCGCTG 1024
 QY 181 TTCTACATGCTGGTGTGTGGCTGACGCTGACCGACTTGTGGGCAAGTCTCTTAC 240
 DB TTCTACATGCTGGTGTGTGGCTGACGCTGACCGACTTGTGGGCAAGTCTCTTAC 1084
 QY 1025 TTCTACATGCTGGTGTGTGGCTGACGCTGACCGACTTGTGGGCAAGTCTCTTAC 1084
 QY 241 CCGGT 300
 DB CCGGT 1144
 QY 1085 CCGGT 1144
 QY 301 GACAACTCGT 360
 DB GACAACTCGT 1204
 QY 1145 GACAACTCGT 1204
 QY 361 CTGCAACTCTGGGCGCATGAGGACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB CTGCAACTCTGGGCGCATGAGGACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1264
 QY 1205 CTGCAACTCTGGGCGCATGAGGACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1264
 QY 421 CGACGGCATATCACTCGGCGCGCTGAGGCGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 DB CGACGGCATATCACTCGGCGCGCTGAGGCGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
 QY 1265 CGACGGCATATCACTCGGCGCGCTGAGGCGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
 QY 481 CTGCGCTTCTGGGCGCTATCTTTCATGAGGCTTGGGAAATTGTGTGTGTGTGTGTGTGTGTGT 540
 DB CTGCGCTTCTGGGCGCTATCTTTCATGAGGCTTGGGAAATTGTGTGTGTGTGTGTGTGTGTGT 1384
 QY 1325 CTGCGCTTCTGGGCGCTATCTTTCATGAGGCTTGGGAAATTGTGTGTGTGTGTGTGTGTGTGT 1384
 QY 541 ACTGTGTCTTATTCAGATGT 600
 DB ACTGTGTCTTATTCAGATGT 1444
 QY 1385 ACTGTGTCTTATTCAGATGT 1444
 QY 601 GTGCTTACTCCAGCTCATGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 DB GTGCTTACTCCAGCTCATGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
 QY 1445 GTGCTTACTCCAGCTCATGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
 QY 661 GCCATGCGCACTCTTATTCAGATGT 720
 DB GCCATGCGCACTCTTATTCAGATGT 1564
 QY 1505 GCCATGCGCACTCTTATTCAGATGT 1564
 QY 721 AGGAGT 780
 DB AGGAGT 1624
 QY 1565 AGGAGT 1624
 QY 781 CTGATGACCTCTGT 840
 DB CTGATGACCTCTGT 1684
 QY 1625 CTGATGACCTCTGT 1684
 QY 841 GTATATGCAATTTTCTTCTGAGTCCCGCGCAAGACACTGTGGAGTGTGTGTGTGTGTGTGTGTGT 900
 DB GTATATGCAATTTTCTTCTGAGTCCCGCGCGCAAGACACTGTGGAGTGTGTGTGTGTGTGTGTGT 1742
 QY 1685 GTATATGCAATTTTCTTCTGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 944
 DB GTATATGCAATTTTCTTCTGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1742
 QY 901 AAAATTTTCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 944
 DB AAAATTTTCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1742
 QY 1743 GGGGCTGTGATTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1786

RESULT 10
 AAF21235

ID AAF21235 standard; DNA; 14607 BP.
XX AAF21235;
AC
XX 14-MAR-2001 (first entry)
DT
XX Human low adenosine antisense oligonucleotide related sequence #2802.
DE
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pain; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000MO-US008020.
XX
XX 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
XX Nyce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
PI
XX
XX Disclosure; Page 1144-1147; 15922P; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors and
CC immunoglobulin and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;
SQ

Query Match 72.5%; Score 848.4; DB 3; Length 14607;
Best Local Similarity 94.4%; Pred. No. 5.1e-191;
Matches 891; Conservative 0; Mismatches 51; Indels 2; Gaps 1;
QY 1 ATGAGTCCGCGTTCTTACCGCTGCGAAGACACCACTCTGTGGAAAAAGGCACTCGCG 60
DB 845 ATGAGTCCGCGTTCTTACCGCTGCGAAGACACCACTCTGTGGAAAAAGGCACTCGCG 904
QY 61 GTGATGGGGGGGTGCTCTTACGACACCGGCTCTCTGGGCAACTGCTGGGCTTGGGGCTG 120
DB 905 GTGATGGGGGGGTGCTCTTACGACACCGGCTCTCTGGGCAACTGCTGGGCTTGGGGCTG 964
QY 121 CTGGGCGGCTGGGGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 180
DB 965 CTGGGCGGCTGGGGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 1024
QY 181 TTCTACATGCTGGTGTGTGGGCTGACGGTCAACGACTTGTGGGCAAGTGCCTTAAGC 240
DB 1025 TTCTACATGCTGGTGTGTGGGCTGACGGTCAACGACTTGTGGGCAAGTGCCTTAAGC 1084
QY 241 CCGGTGTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 1085 CCGGTGTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
QY 301 GACAACTGCTGGTGGCAAGCGCTTGGCTTCTGATGCTCTTGGGGCTGCTGCGACA 360
DB 1145 GACAACTGCTGGTGGCAAGCGCTTGGCTTCTGATGCTCTTGGGGCTGCTGCGACA 1204
QY 361 CTGCAACTCTGCGCAATGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 1205 CTGCAACTCTGCGCAATGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
QY 421 CGACGGCAATACCTTGGGCTGGGCGCACTGTGTGGGCGGCGGCTGTGAGCGCTTCTTC 480
DB 1265 CGACGGCAATACCTTGGGCTGGGCGCACTGTGTGGGCGGCGGCTGTGAGCGCTTCTTC 1324
QY 481 CTGGCTTTTGGGCGCTACCTTTCATGAGGCTTGGGAACTTGTGAGTACTGCGCGG 540
DB 1325 CTGGCTTTTGGGCGCTACCTTTCATGAGGCTTGGGAACTTGTGAGTACTGCGCGG 1384
QY 541 ACCTGTGCTTTATCCAGATGCTGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 1385 ACCTGTGCTTTATCCAGATGCTGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
QY 601 GTGCTTACTCCAGCTTCAATGCGGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 1445 GTGCTTACTCCAGCTTCAATGCGGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504
QY 661 GCGATGCGCAACTCTATGCGATGCAACCGGCGGCTGCAACCGGCGGCTGCTGCTGCTGCTG 720
DB 1505 GCGATGCGCAACTCTATGCGATGCAACCGGCGGCTGCAACCGGCGGCTGCTGCTGCTGCTG 1564
QY 721 AGGSACTGTGCGAGCGCGCGCGAGCGGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 1565 AGGSACTGTGCGAGCGCGCGCGAGCGGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1624
QY 781 CTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 1625 CTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1684
QY 841 GTTATTTGATTTGTTCTGTGATGCTCCCGGCAAGACACCTGGAGTGAAGGCTTGAAG 900
DB 1685 GTTATTTG--TGAATCCCGGGGCGCGAGGGGCGCGCGCGCTGAGGCTGGGGAAG 1742
QY 901 AAACATTTTCACTGCTGCTCTCTCTTCTTCCCAAGTATCGCG 944
DB 1743 GGGGCTCTGGATTGTGGTCT 1786
RESULT 11
AB296929
ID AB296929 standard; DNA; 14607 BP.

XX	AB296929;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human nucleic acid sequence.
XX	
XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	anticholinergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW	adenosine gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX	lung inflammation; respiratory disease; ds.
OS	Homo sapiens.
XX	
XX	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shanabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(e) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 12171; 872bp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' interon-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, anticholinergic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 14607 BD; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;

Query March	72.5%	Score 848.4	DB 10	Length 14607
Best Local Similarity	94.4%	Pred. No. 5.1e-191		
Matches 891	Conservative	0	Mismatches 51	Indels 2
				Gaps 1

QY	Db	QY	Db
ATGAAGTGGCGGTTCTTACCGGTGCGAGAAACAACCTGTGGAAAAAGGCAACTCGGCG	60	61	GTGATGGCGGGGGTGCTCTTTCAGACACCGGCGCTCTTGCGCAACTGTGCGCCCTTGGGGCTTG
ATGAAGTGGCGGTTCTTACCGGTGCGAGAAACAACCTGTGGAAAAAGGCAACTCGGCG	904	905	GTGATGGCGGGGGTGCTCTTTCAGACACCGGCGCTCTTGCGCAACTGTGCGCCCTTGGGGCTTG

[illegible]

RESULT 12
ABD20778
ID ABD20778 standard; DNA; 14607 BP.

AC	ABD20778;
XX	
DT	29-JUL-2004 (first entry)

DE Human pulmonary and inflammatory target DNA #389.
XX
KM Human; antileukine; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cystostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasocostriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension.

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; de.
 OS Homo sapiens.
 PN WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPIS-) EPIGENESIS PHARM INC.
 XX
 PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 XX
 DR WPI; 2003-093058/08.
 XX
 PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 12171; 763pp; English.

CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes (b) a kit that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypertensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;

Query Match 72.5%; Score 848.4; DB 11; Length 14607;
 Best Local Similarity 94.4%; Pred. No. 5,1e-191;
 Matches 891; Conservative 0; Mismatches 51; Indels 2; Gaps 1;

QY 1 ATGAAGTCCCGCTTACCGCTGCGAAGAACACCACTCTGTGAAAAAGCAACTGGGCG 60
 DB 845 ATGAAGTCCCGCTTACCGCTGCGAAGAACACCACTCTGTGAAAAAGCAACTGGGCG 904
 QY 61 GTGATGGGGGGGTGCTTTACGACACCGGCTCTCTGGCAACTGCTGGCCCTCGGGGCTG 120
 DB 905 GTGATGGGGGGGTGCTTTACGACACCGGCTCTCTGGCAACTGCTGGCCCTCGGGGCTG 964
 QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCGTCACTGCGCCGCTGCTCGGCTC 180

DB 965 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCGTCACTGCGCCGCTGCTCGGCTC 1024
 QY 181 TTCTACATGCTGTGTGTGTGGCCGACGCTCACCACTTCTGGGGAAGTCCCTTAAGC 240
 DB 1025 TTCTACATGCTGTGTGTGTGGCCGACGCTCACCACTTCTGGGGAAGTCCCTTAAGC 1084
 QY 241 CCGGTGTGCTGGCTGCTGCTACGCTCAGAACCGGAGTCTCGGGTGTGCTCGCCGATTG 300
 DB 1085 CCGGTGTGCTGGCTGCTGCTACGCTCAGAACCGGAGTCTCGGGTGTGCTCGCCGATTG 1144
 QY 301 GACAACTGCTGTGCGAAGCTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 DB 1145 GACAACTGCTGTGCGAAGCTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1204
 QY 361 CTGCACTCTCTGGCCATGACATGACATGCTGTGCTCTCTCTTCTTCTTCTTCTTCTTCT 420
 DB 1205 CTGCACTCTCTGGCCATGACATGACATGCTGTGCTCTCTCTTCTTCTTCTTCTTCTTCT 1264
 QY 421 CGACGCGACATGACATGCTGTGCGCTGGCGGCGACATGCTGTGCGCGCTTCTTCTTCTTCT 480
 DB 1265 CGACGCGACATGACATGCTGTGCGCTGGCGGCGACATGCTGTGCGCGCTTCTTCTTCTTCT 1324
 QY 481 CTGGCTTTTGGCGCGCTACCTTTTCAATGCGCTTCTGCGAAGTTCGTGCAATCTGCCGCG 540
 DB 1325 CTGGCTTTTGGCGCGCTACCTTTTCAATGCGCTTCTGCGAAGTTCGTGCAATCTGCCGCG 1384
 QY 541 ACTGTGCTTTATTCAGATGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 1385 ACTGTGCTTTATTCAGATGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
 QY 601 GTGCTCTACTCCAGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 1445 GTGCTCTACTCCAGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
 QY 661 GCATGCGGCAACCTTATGAGTGAAGCAACGCGCGCTGCGACGCGGCAACCGCGCTTCTGCACT 720
 DB 1505 GCATGCGGCAACCTTATGAGTGAAGCAACGCGCGCTGCGACGCGGCAACCGCGCTTCTGCACT 1564
 QY 721 AAGGACTGTGCGGAGCGCGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 1565 AAGGACTGTGCGGAGCGCGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1624
 QY 781 CTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 1625 CTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1684
 QY 841 GTATTGCAATTTGTTCTTGAAGTCTCCCGCAAGACACTGGGAGTGAAGCTTGGAG 900
 DB 1685 GTATTG--TGAATCCCGCGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1742
 QY 901 AAACATTTCAAGTGTGCTGCT 944
 DB 1743 GGGGCTGTGATTTGGTCT 1786

RESULT 13
 AAA35105
 ID AAA35105 standard; DNA; 1216 BP.
 XX
 AC AAA35105;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2794.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW anti-allergic; antiasthmatic; cytostatic; analgesic; impeded airway;
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

XX	06-APR-1999;	99US-0127958P.
PR		
XX	(UPEC-) UNIV EAST CAROLINA.	
PA	(NYCE/) NYCE J W.	
XX		
PI	Nyce JW;	
XX		
DR	WPI: 2000-679539/66.	
XX		
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger	
PT	adenosine receptors during metabolism, useful e.g. for treating cancers	
PT	and respiratory obstructions.	
PS	Disclosure: Page 1139; 1592pp; English.	
XX		
XX	The present invention describes low adenosine (A) content antisense	
CC	oligonucleotides and compositions (I) comprising them. In the antisense	
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base.	
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,	
CC	immunosuppressive, antisthmatic, hypotensive and cytostatic activities.	
CC	The antisense oligonucleotides and (I) can be used to down-regulate the	
CC	expression and or activity of target polypeptides associated with	
CC	lung/respiratory disorders and malignancies, such as stimulating and	
CC	activating peptide factors and transmitters, transcription factors,	
CC	immunoglobulins and antibodies, antibody receptors, cytokines and	
CC	chemokines, endogenously produced specific and non-specific enzymes,	
CC	binding proteins, adhesion molecules and their receptors, cytokine and	
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central	
CC	nervous system (CNS) and peripheral nervous and non-nervous system	
CC	receptors, CNS and peripheral nervous and non-nervous system peptide	
CC	transmitters, defensins, growth factors, vasoactive peptides and	
CC	receptors, binding proteins and malignancy associated proteins. The	
CC	antisense oligonucleotides may be used in this way to treat disorders	
CC	including respiratory obstruction (especially pulmonary obstruction	
CC	and/or bronchoconstriction) and/or lung inflammation, allergy (ies) and/or	
CC	surfactant hypoproduction which are associated with a disease or	
CC	condition selected from pulmonary vasoconstriction, inflammation,	
CC	asthma, emphysema, chronic obstructive pulmonary disease (COPD),	
CC	allergies, asthma, impaired respiration, respiratory distress syndrome	
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary	
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),	
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,	
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide	
CC	fragments and antisense oligonucleotides used in the exemplification of	
CC	the present invention	
XX		
XX		
SO	Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;	
	Query Match 72.3%; Score 847; DB 3; Length 1216;	
	Best Local Similarity 100.0%; Pred. No. 4.6e-191;	
	Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ATGAAGTGGCGGTTTACCGGTCGACGAACACCACTCTGTGGAAGGCAACTCGGGG 60	
DB	350 ATGAAGTGGCGGTTTACCGGTCGACGAACACCACTCTGTGGAAGGCAACTCGGGG 409	
OY	61 GTGATGGCGGGGTGCTCTTACGACCGGCTCTGTGGCAACTCGGCTCTGGGAGCTG 120	
DB	410 GTGATGGCGGGGTGCTCTTACGACCGGCTCTGTGGCAACTCGGCTCTGGGAGCTG 469	
OY	121 CTGGCGGCGCTCGGGGCTGGGGGTGTGCTCGCGGCTCCACTGCGCCGCTTGGTGG 180	
DB	470 CTGGCGGCGCTCGGGGCTGGGGGTGTGCTCGCGGCTCCACTGCGCCGCTTGGTGG 529	
OY	181 TTCTACATGCTGGGTGTGAGCTGTACGGGACCGACTGCTGGGCAAGGCTCTCTAAGC 240	
DB	530 TTCTACATGCTGGGTGTGAGCTGTACGGGACCGACTGCTGGGCAAGGCTCTCTAAGC 589	
OY	241 CCGGTGTGTGGCTGCTACGCTAGAACCGGAGCTTGGGAGTCTTGGCCGCGCATTTG 300	
DB	590 CCGGTGTGTGGCTGCTACGCTAGAACCGGAGCTTGGGAGTCTTGGCCGCGCATTTG 649	
OY	301 GACAACTGTGTGCGCAAGCTTGGCTTCTTCAATGCTCTTTGGGCTCTCTCGACA 360	

Db	650	GACAACTGTTGTGCGCAAGCCTTGCCCTTTCTTATGTCCTTTTGAGGCTCTCGACA	709
Qy	361	CTGCAACTCTGCGCATAGGACATGGAGTGTGAGCTCTCCCTTAGGGACACCTTTCTTTAC	420
Db	710	CTGCAACTCTGGGCATAGGACATGGAGTGTGCTCTCCCTTAGGGACACCTTTCTTTAC	769
Qy	421	CGAGGCGCATACACCTCTGCGCTGGGGGACATGGTGGCCCCCGTGGTGAAGCGCTTTGCC	480
Db	770	CGAGGCGCATACACCTCTGCGCTGGGGGACATGGTGGCCCCCGTGGTGAAGCGCTTTGCC	829
Qy	481	CTGGCTTTCTGCGCGCATACCTTTGATGAGGCTTCGGGAAAGTTGCGAGTACTGCCCCGGC	540
Db	830	CTGGCTTTCTGCGCGCATACCTTTGATGAGGCTTCGGGAAAGTTGCGAGTACTGCCCCGGC	889
Qy	541	ACCTGGTCTTTATCCAGATGGTCCACAGAGAGGAGCTCGCTGTGAGTCTGGGGTACTCT	600
Db	890	ACCTGGTCTTTATCCAGATGGTCCACAGAGAGGAGCTCGCTGTGAGTCTGGGGTACTCT	949
Qy	601	GTCCTCTACTCCAGACCTCTCATAGCGCTGCTGCTCTCGCCACCGTGTGTGCACACTGGCG	660
Db	950	GTCCTCTACTCCAGACCTCTCATAGCGCTGCTGCTCTCGCCACCGTGTGTGCACACTGGCG	1009
Qy	661	GCCATGGCGCAACCTCTCATAGCGATGACACCGCGGCTGACAGGGACACCGCGCTCTGCACC	720
Db	1010	GCCATGGCGCAACCTCTCATAGCGATGACACCGCGGCTGACAGGGACACCGCGCTCTGCACC	1069
Qy	721	AGGGACTGTGCGCGAGCGCGCGCGCGAGAGGAGAACGTCCTCCATGACCCCTTGAGAGAG	780
Db	1070	AGGGACTGTGCGCGAGCGCGCGCGCGAGAGGAGAACGTCCTCCATGACCCCTTGAGAGAG	1129
Qy	781	CTGGATCACTCTCTGCTGCTGGGGCTGATGACCGTGTCTTTCACTATGTGTTCTTGCCC	840
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Db	1190	GTAAATTG 1196	
RESULT 15			
ABZ96921			
ID ABZ96921 standard; DNA, 1216 BP.			
AC ABZ96921;			
DT 17-OCT-2003 (first entry)			
DE Human nucleic acid sequence.			
XX Human; antisense; lung dysfunction; nasal airway dysfunction;			
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;			
XX antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;			
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;			
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;			
XX lung inflammation; respiratory disease; ds.			
OS Homo sapiens.			
XX WO200285308-A2.			
PD 31-OCT-2002.			
PF 23-APR-2002; 2002MO-US013135.			
PR 24-APR-2001; 2001US-0286137P.			
XX (EPIG-) EPIGENESIS PHARM INC.			
PI NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;			
PI Miller S, Tang L, Shahabuddin S;			
XX WPI; 2003-229219/22.			

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAse, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 12163; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;

XX Query Match 72.3%; Score 847; DB 10; Length 1216;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-191;

XX Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 350 ATGAAGTCGCGCTTTACCGCTGCGAGAACACCACTGTGAAAAAGGCAACTCGGCG 409
 QY 61 GATGATGGGGGGGGGGGCTTTACGACACCGGCTCTGCGGCAACCTGCTGGGCGCTG 120
 DB 410 GATGATGGGGGGGGGGGCTTTACGACACCGGCTCTGCGGCAACCTGCTGGGCGCTG 469
 QY 121 CTGGCGCGCTCGGAGGCTGAGGTGCTCGCGGCTCACTGCGCCGCTGCGCTC 180
 DB 470 CTGGCGCGCTCGGAGGCTGAGGTGCTCGCGGCTCACTGCGCCGCTGCGCTC 529
 QY 181 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 530 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
 QY 241 CCGGTTGGTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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 DB 710 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
 QY 421 CGACGGGCAATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 770 CGACGGGCAATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
 QY 481 CTGGCTTTCTGCGGCTACCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 830 CTGGCTTTCTGCGGCTACCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
 QY 541 ACCTGGTCTTTATCCAGATGCTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

DB 890 ACCTGGTCTTTATCCAGATGCTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
 QY 601 GTGCTCTACTCCAGCTCATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 950 GTGCTCTACTCCAGCTCATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
 QY 661 GCCATCGCAACCTCTATGCGATGACCGGCGGCTGCGACCGGCACTCCGCTCTGCAAC 720
 DB 1010 GCCATCGCAACCTCTATGCGATGACCGGCGGCTGCGACCGGCACTCCGCTCTGCAAC 1069
 QY 721 AGGACTGTGCGGAGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 1070 AGGACTGTGCGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
 QY 781 CTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 1130 CTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
 QY 841 GTATATTG 847
 DB 1190 GTATATTG 1196

Search completed: April 22, 2005, 12:41:18
 Job time : 716.49 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 12:36:32 ; Search time 220.57 Seconds
(without alignments)
8686.931 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171
Sequence: 1 atgaagtcgcgcgtctacgcg.....acatggaaccagctcgtga 1171

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	83.6	1488	2	US-08-812-203-4
2	979	83.6	1488	3	US-09-300-864-4
3	979	83.6	1488	3	US-09-598-418-4
4	847	72.3	1216	4	US-09-016-434-1474
5	211	18.0	2236	1	US-08-239-431A-3
6	211	18.0	2236	1	US-09-267-423-3
7	209.4	17.9	2372	4	US-09-016-434-1441
8	204.6	17.5	1077	4	US-09-826-509-558
9	204.6	17.5	1077	4	US-08-134-012-5
10	201.8	17.2	1356	1	US-08-520-519-5
11	201.8	17.2	1356	1	US-08-520-519-5
12	201.8	17.2	1356	1	US-09-039-798-5
13	201.8	17.2	1417	1	US-08-134-012-4
14	201.8	17.2	1417	1	US-08-520-519-4
15	201.8	17.2	1417	1	US-09-039-798-4
16	201.8	17.2	1417	4	US-09-016-434-1403
17	201.8	17.2	1488	1	US-08-134-012-6
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25	201.4	17.2	1074	3	US-08-652-446-29
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27	201.4	17.2	2450	2	US-08-461-379A-5

28	201.4	17.2	2450	2	US-08-462-390B-5	Sequence 5, Appl1
29	201.4	17.2	2450	3	US-08-463-074B-5	Sequence 5, Appl1
30	201.4	17.2	2450	3	US-08-465-585C-5	Sequence 5, Appl1
31	201.4	17.2	2450	3	US-08-652-446-5	Sequence 5, Appl1
32	107.2	9.2	1209	4	US-09-826-509-556	Sequence 556, App
33	107.2	9.2	1376	4	US-09-016-434-1361	Sequence 1361, App
34	107.2	9.2	1394	2	US-08-068-729-3	Sequence 3, Appl1
35	107.2	9.2	1394	3	US-09-255-671-3	Sequence 3, Appl1
36	107.2	9.2	1394	3	US-09-355-366-3	Sequence 3, Appl1
37	101.2	8.6	1467	4	US-09-826-509-560	Sequence 560, App
38	101.2	8.6	1958	1	US-08-115-365-1	Sequence 1, Appl1
39	101.2	8.6	1958	1	US-08-586-897-1	Sequence 1, Appl1
40	101.2	8.6	1958	4	US-09-016-434-1380	Sequence 1380, App
41	99	8.5	2442	1	US-08-390-162-5	Sequence 5, Appl1
42	99	8.5	2442	1	US-08-685-945B-5	Sequence 5, Appl1
43	82.6	7.1	2932	4	US-09-016-434-1419	Sequence 1419, App
44	82.6	7.1	2932	4	US-09-054-272-5	Sequence 5, Appl1
45	71.6	6.1	5688	3	US-09-293-170-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-812-203-4
Sequence 4, Application US/08812203
Patent No. 5958723
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: BOYE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,203
FILING DATE: 06-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEX: (908) 594-4720
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-812-203-4
Query Match 83.6%; Score 979; DB 2; Length 1488;
Best Local Similarity 92.2%; Pred. No. 1e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

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QY 1 ATGAAGTCGCGCTTCTACCGCTGCGAGAACACCTCTGTGAAAAAGGCAACTCGGCG 60
DB 350 ATGAAGTCGCGCTTCTACCGCTGCGAGAACACCTCTGTGAAAAAGGCAACTCGGCG 409
QY 61 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGCGCTG 120
DB 410 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGCGCTG 469
QY 121 CTGGCGCGCTCGGGGGCTGGGGTGTCTGGGGGTCTCACTGGGCGCGCTCGCTG 180
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DB 530 TTCTACATGCTGCTGTGTGCTGCTGACGCTGACGCTTGTGCGCAAGTCTCTAAGC 589
QY 241 CCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 590 CCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
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DB 770 CGACGCGCACTGACCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTG 829
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QY 541 ACCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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QY 1141 CAATTCCACTAACATGAAATCCAGTCTGGA 1171
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RESULT 2

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US-09-300-864-4
; Sequence 4, Application US/09300864
; Patent No. 6214972
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOYE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: JOHN W. MALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,864
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-300-864-4

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Query Match 83.6%; Score 979; DB 3; Length 1488;

Best Local Similarity 92.2%; Pred. No. 1e-243; Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

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QY 1 ATGAAGTCGCGCTTCTACCGCTGCGAGAACACCTCTGTGAAAAAGGCAACTCGGCG 60
DB 350 ATGAAGTCGCGCTTCTACCGCTGCGAGAACACCTCTGTGAAAAAGGCAACTCGGCG 409
QY 61 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGCGCTG 120
DB 410 GTGATGGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGCGCTG 469
QY 121 CTGGCGCGCTCGGGGGCTGGGGTGTCTGGGGGTCTCACTGGGCGCGCTCGCTG 180
DB 470 CTGGCGCGCTCGGGGGCTGGGGTGTCTGGGGGTCTCACTGGGCGCGCTCGCTG 529
QY 181 TTCTACATGCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

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D	530	TTCTACATGCTGCTGTGTGTGGCTGACGGTCAACCACTTGCTGGCAAGTCCCTCTTAAC	589
Q	241	CCGGTGTGTGCTGGCTGCTCAAGCTCAGAAACCGAGCTTGGGGTGTGCGCCCGCATTTG	300
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Q	301	GACAACGTGGTGTGCAAGCCCTTGCCCTTTCATGTCCTTTCATGGGTCTGCTCCAGCA	360
D	650	GACAACGTGGTGTGCAAGCCCTTGCCCTTTCATGTCCTTTCATGGGTCTGCTCCAGCA	709
Q	361	CTGCACCTCTGGCCCATGAGCACTGAGAGTGTGGCTCTCCCTTAGAGCAACCTTTCATAC	420
D	710	CTGCACCTCTGGCCCATGAGCACTGAGAGTGTGGGTCTCCCTTAGAGCAACCTTTCATAC	769
Q	421	CGAAGGCAATCACCCCTGCGCTGTGGGCGCATGTGTGGCCCGGGTGTGAGCGCCCTTTCG	480
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Q	481	CTGGCTTTCCTGGCGCTACCTTTCATGAGGCTCTGGGAAATTGTCACAGTACGACCCCGAC	540
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Q	541	ACCTGTGTCTTATTCACATGTCCAAGAGAGGGCTGTGTGTGGGTGTGGGATATCT	600
D	890	ACCTGTGTCTTATTCACATGTGTCCAAGAGAGGGCTGTGTGTGGGTGTGGGATATCT	949
Q	601	GTGCTCTACTCAAGCTCATGAGCGCTGTGCTGTGCTCCGCGCACCGTCTGTGCAACTCGAC	660
D	950	GTGCTCTACTCAAGCTCATGAGCGCTGTGCTGTGCTCCGCGCACCGTCTGTGCAACTCGAC	1009
Q	661	GCCATGCGCAACTCTATGCAATGCAACCGGCGGCTGCAAGCGGCAACCGCGCTCTGCAAC	720
D	1010	GCCATGCGCAACTCTATGCAATGCAACCGGCGGCTGCAAGCGGCAACCGCGCTCTGCAAC	1069
Q	721	AGGACGTGTGCGGAGCGCGCGCGCGGAGGGAGGAAAGGTCCCTCAGCGCCCTGAGAGAG	780
D	1070	AGGACGTGTGCGGAGCGCGCGCGCGGAGGGAGGAAAGGTCCCTCAGCGCCCTGAGAGAG	1129
Q	781	CTGATCACTCTGTGCTGTGGCGCTGATGACCGTGTCTTTCATATGTGTCTGTGCGC	840
D	1130	CTGATCACTCTGTGCTGTGGCGCTGATGACCGTGTCTTTCATATGTGTCTGTGCGC	1189
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D	1399	CAATTCCACTAATCGAATCCAGTCTGTGA	1429

RESULT 3
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; Sequence 4, Application US/09598418
; Patent NO. 6395499
; GENERAL INFORMATION:

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1  APPLICANT: ABRAMOVITZ, MARK
2  BOIE, YVES
3  SAWYER, NICOLE
4  METTERS, KATHLEEN
5  TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
6  SLIPETZ, DEBORAH
7  NUMBER OF SEQUENCES: 4
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: JOHN W. WALLEN, III
10 STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
11 CITY: RAHWAY
12 STATE: NJ
13 COUNTRY: USA
14 ZIP: 07065-0900
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/598, 418
22 FILING DATE: 20-Jun-2000
23 CLASSIFICATION: <Unknown>
24 ATTORNEY/AGENT INFORMATION:
25 NAME: WALLEN III, JOHN W.
26 REGISTRATION NUMBER: 35,403
27 REFERENCE/DOCKET NUMBER: MFL 94/185
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (908)594-3905
30 TELEX: (908)594-4720
31 INFORMATION FOR SEQ ID NO: 4:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1488 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: DNA (genomic)
38 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
39 US-09-598-418-4
40
41 Query Match      83.6% Score 979; DB 3; Length 1488;
42 Best Local Similarity 92.2%; Pred. No. 1e-243;
43 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;
44
45 1 ATGAAGTCGCGCGTCTTACACCGCTGCAGAAACACCACTCTGTGGAAAAAGCACTCGCG 60
46 350 ATGAAGTCGCGCGTCTTACACCGCTGCAGAAACACCACTCTGTGGAAAAAGCACTCGCG 409
47
48 61 GTGATGAGGCGGCGGTGCTTTACAGACCGCGCTCTTGGGCAACCTGTGCGCCCTTGGGCTG 120
49 410 GTGATGAGGCGGCGGTGCTTTACAGACCGCGCTCTTGGGCAACCTGTGCGCCCTTGGGCTG 469
50
51 121 CTGGCGGCGCTCGCGGCGTGGGTGTGCTCGCGGCTCACTGCGCGCGGCTCGCGCTCGGTC 180
52 470 CTGGCGGCGCTCGCGGCGTGGGTGTGCTCGCGGCTCACTGCGCGCGGCTCGCGCTCGGTC 529
53
54 181 TTCTACATGCTGTGTGTGCGCTTGCACGATCACCAGTCTGTGGCAAGTGCCTCTTAAGC 240
55 530 TTCTACATGCTGTGTGTGCGCTTGCACGATCACCAGTCTGTGGCAAGTGCCTCTTAAGC 589
56
57 241 CCGGTGTGCTGCTGCTGCTTACGCTCAGAACCGAGTCTGGGGGTGCTTGGCGCCGCAATTG 300
58 590 CCGGTGTGCTGCTGCTGCTTACGCTCAGAACCGAGTCTGGGGGTGCTTGGCGCCGCAATTG 649
59
60 301 GACAACCTGTGTGCGCAAGCCTTGCCTTCTATATGCTCTTCTTGGGCTCTCTCGACA 360
61 650 GACAACCTGTGTGCGCAAGCCTTGCCTTCTATATGCTCTTCTTGGGCTCTCTCGACA 709
62
63 361 CTGCAACTCTTGGCCATGAGCACTGAGTGTGCTCTCTCTTAAGGCAACCTTTCTTCTAC 420
64 710 CTGCAACTCTTGGCCATGAGCACTGAGTGTGCTCTCTCTTAAGGCAACCTTTCTTCTAC 769
65 421 CGAGCGCAATCAACCTTGGCGCTGGCGCGCACTGTGTGCGCCCGGCTGTGAGCGCTTCTCC 480

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Db 950 GTGCTTACTCCAGCTCTATGCGCTGTCTCTCCCACTGCTGTGCAACTTCGAC 1009
 QY 661 GCCATGCGCAACCTCTATGCGATGACACCGGCGCTGACGGGACCCGGCTCTGACAC 720
 Db 1010 GCCATGCGCAACCTCTATGCGATGACACCGGCGCTGACGGGACCCGGCTCTGACAC 1069
 QY 721 AGGAGCTGTGCGGACCGCGCGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 Db 1070 AGGAGCTGTGCGGACCGCGCGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
 QY 781 CTGATGATCCTCTCTGCTGTGCGGCTCTATGACCGTCTCTTCACTATGTGTCTGTGCC 840
 Db 1130 CTGATGATCCTCTCTGCTGTGCGGCTGTGATGACCGTCTCTTCACTATGTGTCTGTGCC 1189
 QY 841 GTAATTG 847
 Db 1190 GTTAATTG 1196

RESULT 5

US-08-239-431A-3
 ; Sequence 3, Application US/08239431A
 ; Patent No. 5716835

GENERAL INFORMATION:

APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: NOVEL HUMAN EP PROSTAGLANDIN RECEPTOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA

ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/239,431A
 FILING DATE: 05-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned A.
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: ALRGN.053A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176
 TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2296 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 157...1230
 OTHER INFORMATION:

US-08-239-431A-3

Query Match 18.0%; Score 211; DB 1; Length 2296;
 Best Local Similarity 59.4%; Pred. No. 1,6e-44;
 Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

QY 48 AGGCACTGCGCGGTATGAGGCGGGGTGCTTTCAAGACATCCGCTCTGGGCAACTGTCT 107
 Db 219 AGGCGAAGCCCAAGCCATAGCTCCGTCATGTCTGCGCGGGGTCTGGGAACCTCAT 278
 QY 108 GGGCTGGGAGCTGCTGAGCGGCTCGGGGCTGGGGT--GGTGTCTGCGCGCTCACTGCGC 165
 Db 279 AGCATGCGGCTCTGCTGCGCGGCTGCGGGGAGACGTGGGTGACAGCCCGCGGACG 338
 QY 166 CCGCTGCC--CTGCGTCTTACATGCTGTGTGTGAGCTTGACCGTCACTGCTGGG 224
 Db 339 GAGCTCCCTCTCTCTGTTCACAGTGTGTGATCCAGCTGTGTGTACCGACTGTGCTCGG 398
 QY 225 CAAGTCCCTCTTAAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
 Db 399 GACTGCTCTATCAGCCAGT 458
 QY 285 GCTTGGCGCGGATTTGACACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 344
 Db 459 ACTGGCGCC-----GAGAGCGCGCGGTGACACTTCTGCTTGTGCGCATGACCTTCTT 512
 QY 345 TGGGCTCTCTCGACACTGCAACTCTCTGGCCATGTGACCTGAGTGTGTGTGTGTGTGT 404
 Db 513 CAGCTGGGCAAGATGCTCATGCTCTTGGCATGTGCGCTGAGCGGCTACTCTCATCGG 572
 QY 405 GCACCTTTCTTCTACCGACGACATCACTCTGCGCTGCGGCGCACTGTGTGCGCCCGGT 464
 Db 573 GCACCCCTTCTTCTACCGACGACGCGCTCTGCGCTGCGGCGCGCTGCGCTGTGTGTGT 632
 QY 465 GGTGAGCGCTTCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
 Db 633 CATTAATGAGTCT 692
 QY 525 GCAGTATGCGCGCGGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
 Db 693 CAGTATGCGCGCGGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
 QY 585 GGTGCTGGGTAATCTGT 644
 Db 735 ---GACCGCTTACTGCACTGACCTGACCCGACCTGCTGTGTGTGTGTGTGTGTGTGTGT 791
 QY 645 GCTGTGCAACTCTGCGGCACTGTGCAACTGTGCAACTGTGCAACTGTGCAACTGTGCAACT 702
 Db 792 CGCTGCAACTCTGAGT 851
 QY 703 CACCGCGCTCTGCACTGCACTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 762
 Db 852 CGCTGCGGACCTTCTCTGTGGAGTGTGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 911
 QY 763 CTTGAGCCCC---TGGAGAGCTGTGATCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
 Db 912 AAGGATGTCATGCGGAG 971
 QY 819 CTTCATATGTGTCTGT 853
 Db 972 CTTCGCGTGTGTCTGT 1006

RESULT 6

US-09-267-423-3
 ; Sequence 3, Application US/09267423
 ; Patent No. 6395878

GENERAL INFORMATION:

APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: No. 6395878 Human Prostaglandin EP Receptor
 FILE REFERENCE: 17023 DIV CIP
 CURRENT APPLICATION NUMBER: US/09/267,423
 CURRENT FILING DATE: 1999-03-12

EARLIER APPLICATION NUMBER: 09/019,393
EARLIER FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: 08/239,431
EARLIER FILING DATE: 1994-05-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2296
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157)...(1233)
US-09-267-423-3

Query Match 18.0%; Score 211; DB 3; Length 2296;
Best Local Similarity 59.4%; Pred. No. 1.6e-44;
Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

48 AGCAACTCGCGGATGATGGCGGGGCTCTTCAGCAGCGGCTCTCTGAGCACTGCT 107
219 AGCGAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGCTGCGGAACTCAT 278
108 GGGCTGGGGCTGCTGGCGGCTCGGGGCTGGGT--GGTCTGGCGGCTCACTGGC 165
279 AGCACTGGCGCTCTGGCGGCGCTGGCGGAGGTGGGTGACGCCCGCGCAG 338
166 CCGCTGCC-CTCGGCTCTTACATGCTGATGCTGAGCGCTGACGAGTCAAGCTTGTGG 224
339 GAGCTCCCTCTCTCTGTTCCAGTGTGACGAGCTGATGCTGCTGCTGCG 398
225 CAAGTCTCTTAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
399 GAGCTCTCTCTCTCTGTTCCAGTGTGACGAGCTGATGCTGCTGCTGCTGCTGCT 458
285 GCTTGGCGCGCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
459 ACTGGCGCC-----GAGAGCGCGCGGTGACCTTCTTCCGCTGACCTTCTT 512
345 TGGGCTCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 404
513 GAGCTGGCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
405 GCAACCTTCTTCTGACGAGGCAATCACTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 464
573 GCAACCTTCTTCTGACGAGGCAATCACTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 632
465 GGTGAGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
633 CATCTATGACGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
525 GCACTGCTGCGCGGCACTGCTGCTTATCCAGATGCTCAAGAGAGGCTGCTGCTGCT 584
693 CCGATGCTGCGCGGCACTGCTGCTTATCCAGATGCTCAAGAGAGGCTGCTGCTGCT 744
585 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
735 ---GACGCTTACCTGAGCTGATGAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCT 791
645 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
792 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
703 CACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
852 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
763 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
912 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
819 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853

DB 972 CTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 7

US-09-016-434-1441
Sequence 1441, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1441:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9639719
US-09-016-434-1441

Query Match 17.9%; Score 209.4; DB 4; Length 2372;
Best Local Similarity 59.3%; Pred. No. 4.1e-44;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

48 AGCAACTCGCGGATGATGGCGGGGCTCTTCAGCAGCGGCTCTCTGAGCACTGCT 107
219 AGCGAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGCTGCGGAACTCAT 278
108 GGGCTGGGGCTGCTGGCGGCTCGGGGCTGGGT--GGTCTGGCGGCTCACTGGC 165
279 AGCACTGGCGCTCTGGCGGCGCTGGCGGAGGTGGGTGACGCCCGCGCAG 338
166 CCGCTGCC-CTCGGCTCTTACATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 224
339 GAGCTCCCTCTCTCTGTTCCAGTGTGACGAGCTGATGCTGCTGCTGCTGCTGCT 398
225 CAAGTCTCTTAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
399 GAGCTCTCTCTCTCTGTTCCAGTGTGACGAGCTGATGCTGCTGCTGCTGCTGCTGCT 458
285 GCTTGGCGCGCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344

Db	459	ACTGGGAGCC-----GAGAGCCGCGTGGCACTTCTGGCTTGGCCATGACCTTCTT	51.2
Qy	345	TGGGCTCTCTCGACACTGCACTCCTGGGCGATAGCACTGGAATGCTGGCTTCCCTAGG	40.4
Db	513	CAGCTGGGCGAAGATCCTATGCTCTTTCGCAATGGCCCTGGAGCCGCTACTCTTCGATCCG	57.2
Qy	405	GCACCTTCTCTTACGACGCGACATGACCCCTGGGCGCTGGGGGCACTGGTGGCCCGGT	46.6
Db	573	GCACCCCTACTTACACAGCGCGCGCTTCGCGCTCCGGGGGCGCTGGCGCTGCTGCCTGT	63.2
Qy	465	GGTGAAGCGCTTCTCCCTGGCTTTCGCGCGCTACCTTTCATAGGAGCTTCGGGAAGTTCGT	52.4
Db	633	CATCATGACAGTCTCCCTGCTCTTCTGCTCGCTGCGCGCTGCTGACATATGGACAGTACGT	65.2
Qy	525	GCAGTACTGCGCCGCGACCTGGTGTCTTATTCAGATGATTCACAGAGAGGGCTCGCTGTC	58.4
Db	693	CCAGTACTGCGCCGCGGACCTGGGCTTCATCCGGGACCGGGCG-----73.4	73.4
Qy	585	GATGCTGGGGTACTCTGCTCTACTCTCAAGCTCATAGGGCTGCTGCTCTCGCCACCGT	64.4
Db	735	--GACCGGTTCCTGCACTGTACCCACCCCTGCTGCTCTTCTATGTCTCGGTGCT	79.1
Qy	645	GCTGTGCAACTCGGCGCGCATGGCGCAACCTTATATGGCATGCAACCGGCG--GCTGCAGCGG	70.2
Db	792	CGCTTGCACCTTCAGTGTATTTCTCAACTTCATCCGATATCACCGCCCGGAACCGGAGAAAG	85.1
Qy	703	CACCCGCGCTCTGTGACCAAGGAGCTGTGCGAGCCGCGCGCGGACGGAAGGGAAGCGTCC	76.2
Db	852	CGCGTGGGACCTTCCCTGTGGGAGTGGCGCGGGGCGGCCCGGGGCCCGGAGAGAGGGGA	91.1
Qy	763	CCTCAGCCCC---TGGAGGAGCTGATACCTCTGCTGCTGGCGCTGATACCGTGTCT	81.8
Db	912	AAGGTGTTCATAGGCGAGAGACGGAACCACTCATTTCTTGCTATGACCATAC	97.1
Qy	819	CTTACATATGTGTCTCGCCCGTATATGCATTTG	85.3
Db	972	CTTGGCGGTGTCTCTTGGCTTTACGATTTTGG	100.6

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RESULT 8
US-09-293-170-2
; Sequence 2, Application US/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Breyer, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: US/09/293.170
; EARLIER FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081.989
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (300)..(2126)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
; US-09-293-170-2

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	Query Match	17.9%	Score 209.4	DB 3	Length 6446
	Best Local Similarity	59.3%	Pred. No. 6.7e-44		
	Matches 483	Conservative	0	Mismatches 296	Indels 36
				Gaps 6	
QY	48	AGGCAACTGGGCGGATGGGGCGGGGTCCTTTCAGACCGGGCCCTCGGCGCAACTGCT	107		

Db	596	AGGGAAAGCCAGACGANTCAGCTCCGTCATGTTCTCGGCGGGGGGTCGGGAAACCTCAT	655
Qy	108	GAGCCTGGAGGCTGCTGCGCGCCTCGGGGCTGGGCT--GGTCTGGCGGCTTCACCTGCG	165
Db	656	AGCACTGGCGCTGCGGCGCCCTCGCGGGGGAGACGTGGGGGTGACAGCGCGCGCGAG	715
Qy	166	CCGCTGCC-CTCGGCTTTTACATGCTGATGTGGCTTACGGTCAACCCATCTGCTGG	224
Db	716	GAGCTCCCTCCCTTGGTTCACAGCTGATGACGAGGTGATGTTCAACCACTGCTCGG	775
Qy	225	CAAGGCTCCTCTAAGCCCGGATGCTGGGCTGAGCCTAAGCTACAGAACCGGAGCTGCGGGT	284
Db	776	GACCTGCTTATACGCCCGATGGTACTGGCTTTCGATCGCGGAAACAGACCCTGATGGCG	835
Qy	285	GCTTGGCGCCGSCATTGGACAACCTGTTGGTGCACAGCCTTCGCTTTTCATGTCCTTCTT	344
Db	836	ACTGGCGCCC-----GAGAGCCGCGGGGTGACCTACTTGGCTTTCCGCACTGACTTTT	889
Qy	345	TGGGCTCTCTCGACACTGCAACTCTTGGCCATGGACCTGGATGCTGGACTCTCCCTAGG	404
Db	890	CAGCTGAGCCACGATGTCATGCTCTTGCCATGATGGCCCTGGAGGCTACACTTGATCGG	949
Qy	405	GCACCCCTTTCTTCTACCGAGGGCACATCACTTCGCGCTGGGGCGCATGGTGGCCCGGT	464
Db	950	GCACCCCTACTTCTACAGAGGCCCGCTGCTCGGCTCTCGGGGGCTGGCCGTGCTGCTGT	1009
Qy	465	GGTAGGGGCTTTCCTCCCTGGCTTCTGAGGCGCTACCTTTCAATGGGCTTCGGGAAGTTGCT	524
Db	1010	CATTTATGCACTCTCCCTGCTCTCTCTGCTGCGCCCTGCTGGACTATGGGCAAGTACGT	1065
Qy	525	GCAGTACTGCCCCGGGACCTGGTCTTTATTCAGATGGTCCACAGAGAGGGCTCGCTGC	584
Db	1070	CCAGTACTGCCCCGGGACCTGGTCTTCACTTCGCGACGGGCG-----111111	
Qy	585	GGTGGCTGGGATCTCTGCTCTTCACTCCAGCGCTCATGGCGCTGCTGCTTCGCAACGT	644
Db	1112	---GACCGTTACTCGAGAGCTGATACGCAACCTGCTCTGTTTCAATGTTCTCGATGCT	1168
Qy	645	GCTGTGCAACTCGGGCCCATGCGCAACTTATATGCAATGACACCGGCG--GCTGCACGG	702
Db	1169	CGCTGCAACTTCAGTGTCAATTCACAACATCATCCGATGACGCGAGACCGGAGAG	1228
Qy	703	CACCCGGGCTCTGACACAGGAGACTGTGCGAGCCGGCGCGAGACGGAGGGAAAGCTCC	762
Db	1229	CCGCTGGGGAACTTTCCCTGGGCACTGGCGCGGGGCGGCCCGGAGACAGGGGA	1288
Qy	763	CTTACGCC---TGGAGAGCTGGAATCACTCTCTGCTGGCGCTGATGACCGTGT	818
Db	1289	AAAGGTCTCAATGGCGGAGAGACGACACATCAATTCCTCTGCTATCAATGACATCAAC	1348
Qy	819	CTTCACTATGCTTCTCGCGCCGTAATTCGATTTG	853
Db	1349	CTTGGCCGTGCTCTTGGCTTTCACAGATTTTGG	1383

```

: RESULT 9
: US-09-826-509-558
: Sequence 558, Application US/09826509
: Patent No. 6806054
: GENERAL INFORMATION:
: APPLICANT: Lehmann-Bruinema, Karin
: APPLICANT: Lih, I-Lih
: TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
: FILE REFERENCE: AREN-207
: CURRENT APPLICATION NUMBER: US/09/826,509
: PRIOR FILING DATE: 2001-04-05
: PRIOR APPLICATION NUMBER: 60/195,747
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: 09/170,496
: PRIOR FILING DATE: 1998-10-13
: NUMBER OF SEQ ID NOS: 589

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SOFTWARE: PatentIn Version 2.1
SEQ ID NO 558
LENGTH: 1077
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-509-558

Query Match 17.5%; Score 204.6; DB 4; Length 1077;
Best Local Similarity 58.9%; Pred. No. 4.9e-43;
Matches 480; Conservative 0; Mismatches 299; Indels 36; Gaps 6;

48 AGGCACTGGGGGATGGGGGGGATGCTTTACAGACCGGCTCTGGGCAACTGCT 107
63 AGGCGAAGCCAGCCATCAGCTCCCTCATGTTCTGGCCGGGATGGGAACTCAT 122
108 GAGCCCTGGGGCTGCTGGCGCGCTCGGAGGCTGGAGGT--GGTGTCTGGGGGCTCACTGCGC 165
123 AGCATCTGGGGCTGCTGGCGCGCTGGGAGGAGCTGGGGGTGACGCGCGCGCAG 182
166 CGGCTGCC--CTCGGCTTCTAATGCTGGTGGTGGGCTGACGGCTACCGACTTGGG 224
183 GAGCTCCCTCTCTCTTGTTCAGGTGTGGTGGACCGAGCTGGTGTTCACCGACTGCTCG 242
225 CAAGTCCCTCTAAGCCCGGCTGCTGCTGCTACGCTCAGAACCGAGTCTGGG 284
243 GACCTGCCCTCATCAGCCAGTGTACTGGCTTGTAGCGCGGAGCAGACCTGTGGC 302
285 GGTGGCGCCGCGATTGGACAACCTGTTGGCAAGCTTGCGCTTGTATGCTCTT 344
303 ACTGGGCGCC-----GAGAGCGCGCGGTCACCTTACCTTTGGCAATGACCTTCT 356
345 TGGGCTCTCTCGACACTGCAACTCCTGGCCATGAGCACTGAGTGTGCTCTCCCTAG 404
357 GAGCTGGGCAAGTGTCTATGCTCTTGGCCATGAGCCCTGAGGCGCTTACCTCCATGG 416
405 GACCTCTTCTTCTACCGACGCGACATCACCCTGGCGCTGGGGGCACTGCTGCGCG 464
417 GACCCCTTCTTCTACCGACGCGCGCTCTGGCGCTGGGGGCGCTGGCGCTGCTGCT 476
465 GGTGAGCGGCTTCTCTCGCTGGCTTCTGCGCGCTTCTCATGAGGCTTGGGAACTGCT 524
477 CATCTATGAGTCT 536
535 GAGTATGCTGCGCGCGCGCTGCTGCTTATCCAGATGTCTCAAGAGAGGCTCTGCT 584
537 CAGTATGCTGCGCGCGCGCTGCTGCTTATCCAGATGTCTCAAGAGAGGCTCTGCT 578
585 GGTGCTGGGCT 644
579 --GACCGCTTCT 635
645 GGTGCTGCACTCTGCGCGCGCGCGCTTATGAGGCTTATGAGGCTTCTCTCTCTCTCT 702
636 GCGCTGCACTCTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 695
703 CACCGCGCTCTCTGCAACGAGGACTGTGCGAGCGCGCGCGCGAGGAGGAGCTCT 762
696 CGGCTGCGGAGCT 755
763 CTTGAGCGCC--TGGAGAGTGTGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 818
756 AAGGCTGCTCATGAGGAGGAGAGAGAGCAAGATTTCTCTGCTATGACCATCAAC 815
819 CTTCACTATGCT 853
816 CTTGCGGCTGCT 850

RESULT 10
US-08-134-012-5
Sequence 5, Application US/08134012
Patent No. 5516652
GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Sliet, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Wallen
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-134-012-5

Query Match 17.2%; Score 201.8; DB 1; Length 1356;
Best Local Similarity 61.4%; Pred. No. 2.9e-42;
Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

98 GCACTCTGCTGCGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 157
53 GCACTCTATGTTCTGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 112
158 CACTGCGC--CGTGGCGCTGCTTCTATAGTGTGTGTGCTGAGCGCTGAGCG 214
113 CAGGCGAGCG 172
215 ACTTCTGGGCAAGTGTCTCTTAAAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 274
173 ACTTCTGGGCAAGTGTCTCTTAAAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 232
275 GTTCTGCGGCTGCTGCG 334
233 CCTGCTGGGCT--GGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 289
335 TGTCTCTCTTGGGCTCTCTGACATGCAACTCTGCGCATGAGCACTGAGTGTGCG 394
290 TACCTCTCTTGGGCTCTGAGTCTCATGCTCTTGTGCGATGAGCGCGCGCGCGCG 349
395 TCTCCTTGGGCGACCTTCTCTTCAACGAGGCAATCACTGCGCGCGCGCGCGCGCG 454
350 TGGCGGTGAGCCCTTCACTCTACGCGGAGTGAAGGCGCGCGCGCGCGCGCGCG 409
455 TGGCGCGGTGAGCGCGCTTCTCTGAGCTTCTGCGCGCGCGCGCGCGCGCGCGCG 514
410 CGCTGCGAGCATCTACGCGCTTCTGAGTCTCTTCTGCGCGCGCGCGCGCGCGCG 469
515 GGAAGTCTGTGAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 574

Db 470 GCCAACACGAGAGTACTGCCCGGAGCTGTGCTTCTCCGATGCGC-----TGGG 523
Qy 575 GCTCGCTGTGAGTCTGGGGTACTGTGCTCTTCACTCCAGCTTATGAGCGCTGTGCTCC 634
Db 524 CCACAGCGGGGCGGCGCCCTTCTGCTGAGCTACGCGGCTGTGTGAGCTGTGCTG 583
Qy 635 TCGCACCGTGTGTGCACTGTGCGGCGCATGTGCGCACTTATGCGATGCACTGCGGCG 694
Db 584 CTGCGATCTTCTCTGTGCAAGGCTCGGTCACTCTCACTGTGCGGATGTACCGGACG 643
Qy 695 TCGAGCGGACCGCGCTC 713
Db 644 AGAAGCGCCACAGGCTC 662

RESULT 11
US-08-520-519-5
Sequence 5, Application US/08520519

Patent No. 5728808
GENERAL INFORMATION:
APPLICANT: Abramowitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L. Tibbille
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,519
FILING DATE: 29-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tibbille, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 19098DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-520-519-5

Query Match 17.2%; Score 201.8; DB 1; Length 1356;
Best Local Similarity 61.4%; Pred. No. 2,9e-42;
Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

Qy 98 GCACCTGCTGCGCTTGGGGCTCTGCGCGCTGCGGGCTGTGCTGCGCGGCTC 157
Db 53 GCACCTGTATGTTCTGCGCGGTGTGTTGGGCAACGGGCTGCGCTGTGATCTGA 112
Qy 158 CACTGGGC---CGTGGCCTCGTCTTCTTCAATGCTGTGTGTGCTGTGACGCTAC 214
Db 113 CACGGGACCGGCGCCCTCGGCTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 172
Qy 215 ACTTGTGGGCAAGTCTCTTAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 274

Db 173 ACCTGTGGGACACAGTCTCTGAGCCCGGCGGTGTGCTGTGAGCTATGCGGACAGCT 232
Qy 275 GTGCGGGGAGTGTGCGCCCGGATTTGAGCAACTGTGTGTGCAAGCTTGTGCTTCA 334
Db 233 CCTGTCTGGGCT---GGCCGAGGGGCGCCCGCTGTGCGATGCTTGTGCTTGTGCA 289
Qy 335 TGTCTCTTCTTGGGCTCTCTCTGACACTGTGCACTGTGCGCATGTGAGCTGTGAG 394
Db 290 TGAATCTTCTTGGGCTGTGCGGCTGTGATGTATCTCTTGTGCAATGCGGAGGCTG 349
Qy 395 TCTTCTTGGGACCTCTTCTTCTTACCGAGGACATCACTTGTGCGGCTGTGAG 454
Db 350 TGGCGCTGAGCCACCTCTTCTTACCGGAGCTGTGAGCGGCGGCGGCGGCTGTG 409
Qy 455 TGGCGCGGTGTGAGGCGCTTCTCTGCGCTTGTGCGGCTTGTGAGGCTTGTG 514
Db 410 CGCTGCGAGCATCTACGCTTCTGTGCTTCTTGTGCGGCTGTGCGGCTGTG 469
Qy 515 GGAAGTCTGTGACATCTGCGCGGACCTGTGCTTATTCAGATGTGCAAGAGAG 574
Db 470 GCCAACACGAGAGTACTGCGCGGAGCTGTGCTTCTCTCGGATGCGC-----TGGG 523
Qy 575 GCTCGCTGTGAGTCTGGGGTACTGTGCTCTTACTTCACTTCACTGAGCGCTGTGCT 634
Db 524 CCACAGCGGGGCGGCGCCCTTCTGCTGAGCTTACCGCGGCTGTGCGCTGTG 583
Qy 635 TCGCACCGTGTGTGCACTGTGCGGCGCATGTGCGCACTTATGCAATGCACTGCGG 694
Db 584 CTGCGATCTTCTCTGTCAAGGCTGTGCTGCTCACTCTCACTGTGCGGATGTACCG 643
Qy 695 TCGAGCGGACCGCGCTC 713
Db 644 AGAAGCGCCACAGGCTC 662

RESULT 12

US-09-039-798-5
Sequence 5, Application US/09039798
Patent No. 6365360

GENERAL INFORMATION:
APPLICANT: Abramowitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,798
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,519
FILING DATE: 29-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19098DB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905

TELEFAX: (732) 594-4720
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1356 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-039-798-5

Query Match 17.2%; Score 201.8; DB 3; Length 1356;
 Best Local Similarity 61.4%; Pred. No. 2.9e-42;
 Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

98 GCAACCTGCTGGCCCTGCGGAGCTGTCGCGCGCTGCGGAGTGGGTGCTCGCGCGCTC
 53 GCAACCTGATGTTGTCGTCGCGGAGTGGTGGGCAACGCGGCTGCGCGGATCTGAGCG
 158 CACTGCGCC--CGTGCCTCGGCTTTTCTACATGCTGTGTGTGCTGACGCTACCG
 113 CACGGGACCGGCGCGCCCTCGGCTTGCAGGCTGCTGATCACCGGACTGCGCGCACCG
 215 ACTGTGTGGGCAAGTGCCTCTAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 173 ACTGTGTGGGCAAGTGCCTCTAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 275 GTCTGTGGGCTGT
 233 CCTGTGTGGGCT--GCGCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 335 TGTCTTCTTTTGGGCTCTCTGTGACACTGCACTCTCTGCGCATGAGCACTGAGTGTGCT
 290 TGAACCTTCTTGGCTGTGCGTGCATGCTCATCTTGTGCGCATGAGCGCGCTGCG
 395 TCTCCCTAGGCGACCTTTCTTCTTACGAGGCAATACCTGCGCGCGCGCGCGCGCGCG
 350 TGGCGCTGAGCGACCTTCTTCTTACGAGGCAATACCTGCGCGCGCGCGCGCGCGCGCG
 455 TGGCGCGCGTGTGAGCGCGCTTCTCTGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCG
 410 CGCTGCAACCATCTACGCTTCTGCTGTCTTCTGCGCGCTTCTGCGCGCTTCTGCGCG
 515 GGAAGTGTGAGTACTGCG
 470 GCGAAGCAGCAGTACTGCG
 575 GCTGCTGTGCGTGTGCG
 524 CCGAGCG
 635 TCGCCACCGTGTGCTGCAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 584 CTGCGATCTTCTCTGCAAGGCTGCGGTACCTCAAGCTTGTGCGCGCGCGCGCGCGCG
 695 TCGAGCGGACCGCGCGCTC 713
 644 AGAAGCGCACCGCGCGCTC 662

RESULT 13
 US-08-134-012-4
 Sequence 4, Application US/08134012
 Patent No. 5516652
 GENERAL INFORMATION:
 APPLICANT: Abramowitz, Mark
 APPLICANT: Bole, Yves
 APPLICANT: Grygorczyk, Richard
 APPLICANT: Metters, Kathleen
 APPLICANT: Rushmore, Thomas H.
 APPLICANT: Slidetz, Deborah M.
 TITLE OF INVENTION: DNA ENCODING PROTAGLANDIN RECEPTOR IP
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:

ADDRESSEE: John Wallen
 STREET: 126 E. Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134,012
 FILING DATE: 06-OCT-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Wallen, John W
 REGISTRATION NUMBER: 35,403
 REFERENCE/DOCKET NUMBER: 19098
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3905
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1417 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-134-012-4

Query Match 17.2%; Score 201.8; DB 1; Length 1417;
 Best Local Similarity 61.4%; Pred. No. 3e-42;
 Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

98 GCAACCTGCTGGCCCTGCGGAGCTGTCGCGCGCTGCGGAGTGGGTGCTCGCGCGCTC
 115 GCAACCTGATGTTGTCGTCGCGGAGTGGTGGGCAACGCGGCTGCGCGGATCTGAGCG
 158 CACTGCGCC--CGTGCCTCGGCTTTTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT
 175 CACGGGACCGGCGCGCCCTCGGCTTGCAGGCTGCTGATCACCGGACTGCGCGCACCG
 215 ACTGTGTGGGCAAGTGCCTCTAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 235 ACTGTGTGGGCAAGTGCCTCTAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 275 GTCTGTGGGCTGT
 295 CCTGTGTGGGCT--GCGCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 335 TGTCTTCTTTTGGGCTCTCTGTGACACTGCACTCTCTGCGCATGAGCACTGAGTGTGCT
 352 TGAACCTTCTTGGCTGTGCGTGCATGCTCATCTTGTGCGCATGAGCGCGCTGCG
 515 GGAAGTGTGAGTACTGCG
 470 GCGAAGCAGCAGTACTGCG
 575 GCTGCTGTGCGTGTGCG
 524 CCGAGCG
 635 TCGCCACCGTGTGCTGCAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 586 CCGAGCG
 646 CTGCGATCTTCTCTGCAAGGCTGCGGTACCTCAAGCTTGTGCGCGCGCGCGCGCGCGCG

Query Match	17.2%;	Score 201.8;	DB 3;	Length 1417;
Best Local Similarity	61.4%;	Pred. No. 3e-42;		
Matches 380;	Conservative	0;	Mismatches 227;	Indels 12;
				Gaps 3;

QY	98	GCACACTGCGTGGCCCTGGGGGCTGCTGGGCGCTGGGGGCTGGGGGAGGAGCTCGCGGCTC	157
Db	115	GCACCTGATGTTCTTGCGCCGGGTGGTGGGCAACGGGCTGGCCCTGGGCATCTTAGCG	174
QY	158	CACCTGCGCC---CGTCGCTCGGTCCTTCTACATGCTGGTGTGGCCCTGACGGTCAACG	214
Db	175	CACGGCGACCGGGCGGCCCTCGGCTTCGCGGATCTGGTCAACGGACTGGCGGCGCACCG	234
QY	215	ACTTGGTGGGCAAGTGCCTCTTAAGCCCGGATGATGCTGGCTGCTTAAGCTCAAAACCGA	274
Db	235	ACCTGCTGGGCAACAGCTTCCTGAACCCGGCCGGTGTGTGGCTTAAGCCGCAACAGCT	294
QY	275	GTCCTGGGGTGCCTMGCGCCCGCATTTGAGCAACTCGTTGTGCAAGCCCTTGCTCTTCA	334
Db	295	CCCTGCTGGGCT---GGCCGAGGGCGGCCCGCCCTGTGGAGATGCTTGGCTTGGCCA	351
QY	335	TGTCTTCTTTTGGGCTCTCTCGACACTGCACTCTCGGCAATGAGACTGGAGTCTGGC	394
Db	352	TGACCTTCTTGGGCTGGCGTGCATGCTCATCTCTTGGCATGAGCGTGGAGGCTGGC	411
QY	395	TCTCCCTAAGGGAACCCCTTCTCTTACCCAGCGGCAATACCCCTGGCTGGGCGCACTGG	454
Db	412	TGGCGCTGAGCCACCCTTACTCTTACGGGAGAGTGGAGGGGCCCGCTGGGCCCTGG	471
QY	455	TGGCCCCGGTGGTGAAGCGCTCTCCCTGAGCTTTTCTGCGCGCTACTTTCATGGGCTTCG	514
Db	472	CGGTGCAAGCATATACGCTCTTCTGGGTCTCTTCTGGCGGCTGCCCTGTGGGCTTGG	531
QY	515	GGAGTTCTGCAATATGTCGCCCGGCACTGGTCTTTATCAAGTGTCAAGAGAG	574
Db	532	GCCAACACAGAGATATGCCCCCGGAGCTGGTGTCTTCTCCGATGGGC-----TGGG	585
QY	575	GCTCGCTGTGCGGTGCTGGGGTACTCTGTGCTTACTACAGCTCATGGGCTMGCTGGTCC	634
Db	586	CCGACGCGGGCGGCGCGCTTCTGTGCTGACCTTACGCGGCGCTGGTGGCCCTGCTGGTGG	645
QY	635	TGCGCACGCTGTGTGCAACTTCGAGCGCATGCGCACTTATGCAATGCAATGCAACCGAGC	694
Db	646	CTGCGATCTTCTCTGCAACGAGCTGATCAACCTCAGGCTCTGCGCATGACGCGCAGC	705
QY	695	TGAGAGGGAACCCGCGCTC	713
Db	706	AGAGGCGCACAGAGGCTC	724

Search completed: April 22, 2005, 18:00:07
Job time : 226.57 secs

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QY 285 GCTTGGCCCGGCAATTGGACAATCTGTGTGCAAGCCTTGCCCTTCTTCAATGTCTTCTT 344
DB 459 ACTGGGGCC-----GAGAGCCGCGGTGCACTTCTGCTTCTTCCATGACCTTCTT 512
QY 345 TGGGCTCTCTGACACTGTGCACTCCCTGCGCATGGACATGGAGTGGCTCTCCCTAGG 404
DB 513 CAGCTGGCCACAGATGTCTATGCTCTTGGCATGGCCCTGAGCGCTACTCTCTGATCGG 572
QY 405 GCACCCCTTCTTCAACGACGACATCAACCTGCGCTGGGCGCATGCTGGCCCCGGT 464
DB 573 GCACCCCTTACTTACACAGCGCGGCTCTGGGCTCTGGGCGCTGGCCGCTGCTGT 632
QY 465 GGTGAGCGCTTCTCCCTGCTTCTGCGGCTACTCTTCAATGAGCTTCGGAATTCGT 524
DB 633 CATCTATGCAGTCTCCCTGCTCTTCTGCTGCTGCGCTGCTGACTATGGCAGTACGT 692
QY 525 GCAGTACTGCCCCGGGACCTGCTGCTTATCCAGATGTCCACAGAGAGGCTGCTGTG 584
DB 693 CCAGTACTGCCCCGGGACCTGCTGCTTCAATCCGCAAGGGCG----- 734
QY 585 GGTGCTGGGGTACTGTGTCTACTCAAGCTCATGCGCTGCTGCTCGCCACCGT 644
DB 735 ---GACCGCTTACTGTGCAAGCTGTAAGGCAACCTGCTGCTTCTCATTTGTCTGGTGT 791
QY 645 GCTGTGCAACTTGGCGCCATGGCGCAACTCTATGCGATGACCGGG--GCTGCAAGCG 702
DB 792 CGCTGTCAACTTCAATGTCTATCTCAACCTCATCCGATGCAACGCGCAAGCGGAGAG 851
QY 703 CACCGCGGCTCCGCAACGAGGACGTGCGGAGCGGCGGCGGAGGAGGAGGTCC 762
DB 852 CCGCTGCGAATCTTCCCTGGGCAATGCGCCGAGGCGGCCCGGAGCGGAGAGGGA 911
QY 763 CCTCAAGCCCC--TGAAGAGCTGATCACTCTGCTGCTGCGCTGATGACCGTGT 818
DB 912 AAGGATGTCCATGGGAGAGAGAGGAGACCACTCATTTCTCTGCTATCATGACATCAC 971
QY 819 CTTCACTATGTGTCTCTGCGCGTAATTGCATTG 853
DB 972 CTTGCGCGTGTGCTCTGCTTTCACGATTTTG 1006

Search completed: April 22, 2005, 21:25:19
Job time : 777.996 secs

Db 735 -----GACGGCTTACCTGACAGTGTATGCGACACCTGCTGCTCTCTCATTTGCTCGAGTCT 791
Qy 645 GCTGTGCAACTGTGGCGCCATGCGCAACTCTATGCGATGACCGGGCG--GCTGCAAGCGG 702
Db 792 CGCTGTCAACTTCAAGTGTATCTTCAACCTTCATCCGATGCAACCGCGCGAAGCGGAAAG 851
Qy 703 CACCGCGCTCTCGCAACAGGAGCTGTGCGGACCGCGCGCGGACCGGAGGAGAGGTCTC 762
Db 852 CGCTGTGCAACTTCTCTGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGGGA 911
Qy 763 CCTCAAGCCCC--TGAGAGAGCTGTGATCACTCTGCTGTGCTGCGCTGTGACCGTGTCT 818
Db 912 AAGGCTGTCAATGCGGAG 971
Qy 819 CTTCATGATGTGTCTCTGCTGCGCGCTTAATGCAATTTG 853
Db 972 CTTCGCGCTGTCTCTGCTCTTTCACGATTTTGG 1006

RESULT 14

US-10-305-720-1441
; Sequence 1441, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1441
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Genbank ID No. US20040010136A1 g639719
US-10-305-720-1441

Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;
Qy 48 AGGCACTGCGCGGTGATGCGCGGTGCTCTTACAGACCGGCTCTGCGCAACCTGCT 107
Db 219 AGGCGAAAGCCGACGATACGCTCCGTCATGTTCTGCGCGGGGTGCTGCGGAACTCAT 278
Qy 108 GCGCTGTGGGCTGTGCGCGGCTCGGAGCTGTGGGT--GGTCTCGCGGCTCCACTGCGC 165
Db 279 AGCACTGTGCGTGTGCGCGCGCTGCGCGGAGAGTGGGTGTGAGCGCCGCGCGAG 338
Qy 166 CCGCTGCC--CTGCGTCTTCTACATGCTGTGTGTGCGCTGACGCTACGAGTCTGTGCGG 224
Db 339 GAGCTCTCTCTCTTGTTCACGTGTGTGTGACCGAGCTGTGTTCACGACTGTCTCG 398
Qy 225 CAGTGTCTCTTACGCGCGGT 284
Db 399 GAGCTGTCTTATAGCCAGT 458
Qy 285 GCTTGTGCGCGCATTTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 344
Db 459 ACTGTGGCGCC-----GAGAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
Qy 345 TGGGCTCTCTGTGACACTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 404
Db 513 CAGCTGT 572
Qy 405 GCACTCTTCTTCTTACGAGGAGCAATCACTGTGCGCTGTGCGGCACTGTGTGCGCCCGGT 464

Db 573 GCACCTTACTTCTTACAGAGCGCGGTCTGCGCTTCGCGGAGCGCTGCGCGCTGCTGT 632
Qy 465 GGTGAGCGCTTCTCTCCCTGCTTCTGCGGCTTACCTTTATGAGGCTTGAGGAATGCT 524
Db 633 CATCTAGAGTGTCTCTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
Qy 525 GCAGTATGCGCGCGACCTGT 584
Db 693 CCAATGTCTCCCGGAGCTGT 734
Qy 585 GGTGTGAGTACTGT 644
Db 735 ---GACCGCTTACCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
Qy 645 GCTGTGCAACTGTGGCGCATGCGCACTCTATGAGATGACCGGCG--GCTGCAAGCGG 702
Db 792 CGCTGTCAACTTCAAGTGTATCTTCAACTCATCCGATGACCGCGCGAGCGGAGAG 851
Qy 703 CACCGCGCTCTGCAACAGGAGTGTGCGGCGCGCGCGCGCGCGGAGGAGAGCTGCTC 762
Db 852 CGCTGTGCGACCTTCCCTGTGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGAGAGGGA 911
Qy 763 CCTCAAGCCCC--TGAGAGAGCTGTGATCACTCTCTGCTGTGCGCTGTATGACCTGTCT 818
Db 912 AAGGCTGTCAATGCGGAG 971
Qy 819 CTTCATGATGTGTCTCTGCTGCGCGCTTAATGCAATTTG 853
Db 972 CTTCGCGCTGTCTCTGCTCTTTCACGATTTTGG 1006

RESULT 15

US-10-755-889-91
; Sequence 91, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-91

Query Match 17.9%; Score 209.4; DB 18; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;
Qy 48 AGGCACTTCTGCGGTGATGCGCGGTGCTCTTACAGACCGGCTCTGCGCAACCTGCT 107
Db 219 AGGCGAAAGCCGACGATACGCTCCGTCATGTTCTGCGCGGGGTGTGCGGAACTCAT 278
Qy 108 GCGCTGTGGGCTGTGCGCGGCTCGGAGCTGTGGGT--GGTGTCTGCGGCTCCACTGCGC 165
Db 279 AGCACTGTGCGTGTGCGCGCGCTGCGGAGAGAGTGGGTGTGAGCGCCGCGCGAG 338
Qy 285 GCTTGTGCGCGCATTTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 344
Db 459 ACTGTGGCGCC-----GAGAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
Qy 345 TGGGCTCTCTGTGACACTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 404
Db 513 CAGCTGT 572
Qy 405 GCACTCTTCTTCTTACGAGGAGCAATCACTGTGCGCTGTGCGGCACTGTGTGCGCCCGGT 464

TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157) ... (1233)
US-10-352-684A-35

Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

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QY 48 AGGCACTGCGGGGATATGAGCGGGGCTCTTACAGACCGGCTCTCTGAGCAACTGCT 107
DB 219 AGGCGAAAGCCAGCCATCAAGCTCCGATGTTCTCGCGGGGTGCTGAGAACTCAT 278
QY 108 GGCCTTGGGCTCTGCGCGCTCGGGCTGGGGT--GGTCTCGCGGCTTCACTGCG 165
DB 279 AGCATGCGCTCTGCGCGCGCGCTGGCGGGAGCTGGGGGTCAGCCCGCGCGAG 338
QY 166 CCGCTGCC--CTGGGTCTTCAATGCTGTGTGTGTGGCTTACGAGTCACTTGG 224
DB 339 GAGCTCCCTCTCTTGTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398
QY 225 CAAGTCCCTCTTAAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 399 GACCTGCTCATGAGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
QY 285 GCTTGGCGCCGATGGAACAATGTTGTGCAAGCCCTTCTTCAATGCTTCTT 344
DB 459 ACTGGGGCC-----GAGAGCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
QY 345 TGGGCTCTCTGACACTGCACTGCTGCGCATGGAAGTGTGTGTGTGTGTGTGT 404
DB 513 GACCTGCGCACATGCTCATGCTTCTGCGCATGCGCTGAGAGGCTTCACTTGT 572
QY 405 GACCTTCTTCTTACCGAGGCAATCACTGCGCTGCGGCGCACTGTGTGTGTGT 464
DB 573 GACCCCTTCTTCTTACCGAGGCGCGCTGCGCTGCGGCGCGCTGTGTGTGTGT 632
QY 465 GGTGAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 524
DB 633 CATCTATGAGTCTCTCTGCTTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGT 692
QY 525 GAGTATCTGCGCGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
DB 693 CAGTATGCGCGGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 744
QY 585 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
DB 735 ---GACCGCTTACCTGCACTGCACTGCACTGCTGTGTGTGTGTGTGTGTGT 791
QY 645 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 702
DB 792 CGCTGTCAATGATGTCTTCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
QY 703 GACCGCGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 762
DB 852 CGCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 911
QY 763 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
DB 912 AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
QY 819 CTTCACTATGTTCTTCTGCGCGGTAATGTGATTTG 853
DB 972 CTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006
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RESULT 13
US-10-366-288-35
Sequence 35, Application US/10366288
Publication No. US2003021628A1
GENERAL INFORMATION:

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APPLICANT: Powell, Douglas  
APPLICANT: Welch, Nadine S.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,  
TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 12825, 9952, 5816,  
TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,  
TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES  
FILE REFERENCE: MP102-025P1RNMNM  
CURRENT APPLICATION NUMBER: US/10/366,288  
CURRENT FILING DATE: 2003-02-13  
PRIOR APPLICATION NUMBER: 60/357,391  
PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: 60/380,249  
PRIOR FILING DATE: 2002-05-13  
PRIOR APPLICATION NUMBER: 60/391,306  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: 60/406,297  
PRIOR FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: 60/412,007  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: 60/417,508  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 60/432,318  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 35  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-366-288-35
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Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

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QY 48 AGGCACTGCGGGGATATGAGCGGGGCTCTTACAGACCGGCTCTCTGAGCAACTGCT 107
DB 219 AGGCGAAAGCCAGCCATCAAGCTCCGATGTTCTCGCGGGGTGCTGAGAACTCAT 278
QY 108 GGCCTTGGGCTCTGCGCGCTCGGGCTGGGGT--GGTCTCGCGGCTTCACTGCG 165
DB 279 AGCATGCGCTCTGCGCGCGCGCTGGCGGGAGCTGGGGGTCAGCCCGCGCGAG 338
QY 166 CCGCTGCC--CTGGGTCTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 224
DB 339 GAGCTCCCTCTCTTGTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398
QY 225 CAAGTCCCTCTTAAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 399 GACCTGCTCATGAGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
QY 285 GCTTGGCGCCGATGGAACAATGTTGTGCAAGCCCTTCTTCAATGCTTCTT 344
DB 459 ACTGGGGCC-----GAGAGCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
QY 345 TGGGCTCTCTGACACTGCACTGCTGCGCATGGAAGTGTGTGTGTGTGTGTGT 404
DB 513 GACCTGCGCACATGCTCATGCTTCTGCGCATGCGCTGAGAGGCTTCACTTGT 572
QY 405 GACCTTCTTCTTACCGAGGCAATCACTGCGCTGCGGCGCACTGTGTGTGTGT 464
DB 573 GACCCCTTCTTCTTACCGAGGCGCGCTGCGCTGCGGCGCGCTGTGTGTGTGT 632
QY 465 GGTGAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 524
DB 633 CATCTATGAGTCTCTCTGCTTCTTCTGCTGTGTGTGTGTGTGTGTGTGTGT 692
QY 645 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
DB 912 AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
QY 819 CTTCACTATGTTCTTCTGCGCGGTAATGTGATTTG 853
DB 972 CTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006
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Db 723 ---GACCGCTTACCTGACAGCTGTAACGCAACCCCTGCTGCTTCTCATGTTCTCGGTGCT 789
QY 645 GCTGTGCAACCTCGGCGCATGCGCAACCTTATGAGATGCAACCGGCG--GCTGACGCG 702
Db 790 CGCCTGCAACTTCAAGTATTTCTCAACCTTCACCTGACACCGCGCAAGCGGAG 849
QY 703 CACCCGCGCTCTGCAACGAGGACTGTGCGAGCCGCGCGGAGCGGAGAGCGTCC 762
Db 850 CCGCTGCGGACCTTCCCTTGGGAGTGGCCGCGGCGCGCCCGCGGAGAGAGAGGA 909
QY 763 CCTGACGCCCC--TGAGAGAGCTGATGATCACTCTGCTGCTGCTGCTGATGACCTGCT 818
Db 910 AAGGCTGTCATGCGGAGAGACCGACCACTTCTCTGCTATGATGACATCAC 969
QY 819 CTTCACTATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 970 CTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004

RESULT 11
US-10-225-567A-290
; Sequence 290, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roubert, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 290
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-290

Query Match 17.9%; Score 209.4; DB 15; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;
QY 48 AGCAACTGCGCGGTGATGAGCGGCGGTGCTTTCAGACACCGGCTTCGCGCAACTGCT 107
Db 219 AGCGGAAAGCCAGCATGAGTCCGTCATGTTCTGCGCGGCGGTGCTGCGGAACTCAT 278
QY 108 GCGCTGCGGCTGCTGCGCGCGCTGCGGCGGTGCTGCGGCGGTGCTGCGGCGGT 165
Db 279 AGCACTGCGGCTGCTGCGCGCGCTGCGGCGGAGAGTGGAGGTGAGCGCGCGGAG 338
QY 166 CCGCTGCGC--CTGCGGTCTTTCATGATGCTGATGCTGATGCTGATGCTGATGCTG 224
Db 339 GAGCTGCTGCTGCTTTCATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 398
QY 225 CAAGTCTCTCTAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
Db 399 GACCTGCTCTATGAGCCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
QY 285 GCTTGGCGCGGCTGAGCACTGCTTGTGCGCAAGCTTCCCTTTCATGCTGCTTCT 344
Db 459 ACTGGGCGCC---GAGAGCGCGCGTGAACCTTTCCTTTCATGCTGCTTCTTCT 512
QY 345 TGGGCTCTCTGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
Db 513 CAGCTGCGCAAGATGCTATGCTTTCGCGATGCGCTGAGCGCTTCTGATGCTG 572
QY 405 GAACCTTTCTTCTACGAGCGGACATCACTTGGCGCTGCGGCGCACTGCTGCGGCT 464
Db 573 GAACCCCTACTTCTACGAGCGCGCTGCTGCGGCGCTGCGGCGCGCTGCTGCTGCT 632

QY 465 GGTAGCGCTTCTCCCTGCGCTTTCGCGCGCTACCTTTCATGCTTCCGGAAGTTCGT 524
Db 633 CATCTATGAGTCTTCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
QY 525 GCAGTACTGCGCGGACCTGCTGCTTTCATGATGCTGCTGCTGCTGCTGCTGCTGCT 584
Db 693 CAGTACTGCGCGGAGCTGCTGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
QY 585 GGTGCTGCGGCTGCTGCTGCTTACTGAGCTTCAATGAGCGCTGCTGCTGCTGCTGCT 644
Db 735 ---GACCGCTTACCTGCAAGCTGATGAGCACTGCTGCTGCTGCTGCTGCTGCTGCT 791
QY 645 GCTGTGCAACCTGCGCGCATGCGCAACCTTATGAGATGACCGGCG--GCTGACGCG 702
Db 792 CGCCTGCAACTTCAAGTATTTCTCAACCTTATCCGATGACACCGCGAGCGGAGAG 851
QY 703 CACCCGCGCTCTGCAACGAGGACTGTGCGAGCCGCGCGGAGCGGAGGAGAGCGTCC 762
Db 852 CCGCTGCGGACCTTCCCTGCGGAGTGGCCGCGGCGCGCCCGGAGCGGAGAGAGGGA 911
QY 763 CCTGAGCCCC--TGAGAGAGCTGATGATCACTCTGCTGCTGCGGCTGATGACCTGCT 818
Db 912 AAGGCTGTCATGCGGAG 971
QY 819 CTTCACTATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 972 CTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 12
US-10-352-684A-35
; Sequence 35, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1RMONIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2372

PRIOR APPLICATION NUMBER: 08/239,431
PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2296
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157)...(1233)
US-10-108-714-3

Query Match 18.0%; Score 211; DB 13; Length 2296;
Best Local Similarity 59.4%; Pred. No. 3e-51;
Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

48 AGGCACTGGGGGATGAGTGGGGGCTCTTACAGACCGGCTCTCTGGGCAACCTGCT 107
219 AGGCGAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGCTGCGGAACTCAT 278
108 GGGCTGGGGCTGCTGCGCGCTCGGGGCTGGGGT--GGTCTGCGGGCTCCACTGCGC 165
279 AGACTGGGCTGCTGCGCGCTGCGGGGACGTGGGGGACAGCCCGCGCGAG 338
166 CCGCTGCC-CTGGCTCTTACATGCTGTGTGTGCTGACGGTCAACGACTTGTGGG 224
339 GAGCTCCCTCTCTTTCACACGTGTGACCGAGCTGTGTTCACCACTGCTCGG 398
225 CAAGTCTCTTAAAGCCGGTGGTGGCTGCTACGCTACAGACCGGAGTCTGGGGT 284
399 GACTCTCTTACAGCCAGTGTGCTGTGACGGGAAACCGCTGGTGGC 458
285 GCTTGGCGCCGATGAGCACTGTTGTSCAAAGCTTGGCTTCTTCACTGCTTCT 344
459 ACTGGGGCC-----GAGAGCGCGCGGTSCACTTCTTGGCCATGACTTCTT 512
345 TGGGCTCTCTGACACTGCACTCTGCG-CATGAGCACTGAGTGTGCTCTCTAGG 404
513 GAGCTTGGCAGCATGCTCATGCTTTCG-CATGAGCCCTGAGACGCTTCTCATGCG 572
405 GACCCCTTCTTCTACAGAGGCACTGACCTGCGCTGGGGGCACTGTGAGCCCGCT 454
573 GACCCCTTCTTCTACAGAGGCACTGACCTGCGCTGGGGGCACTGTGAGCCCGCT 632
465 GGTGAGCGCTTCTCTGCTGCTTCTGCGGCTTCTTCACTGAGGCTTGGGAACTTCT 524
633 CATCTATGAGTCTCTCTGCTTCTGCTGTGCTGCGCTGCTGACTATGAGGAGTAC 692
525 GAGTACTGCGCGGACCTGCTGCTTATTCAGATGTGTCCAGAGAGGAGCTCGCTGTC 584
693 CAGTACTGCGCGGAGCTGCTGCTTCAATCCGCAAGGAGG-----724
585 GGTGCTGGGGTACTGTGTCTCTACTTCACTGCACTGAGGCTGCTGCTGCTGCTGCT 644
735 ---GACCGGCTTACCTGCACTGAGCCACCTGCTGCTGCTTCTATGCTCTGAGTCT 791
645 GCTGTGCAACTCTGCGGCACTGAGCACTCTATGAGTACCGGAGG--GCTGAGCGG 702
792 CGCTGCACTTCACTGCTCTTCTTCACTGAGTACCGGAGGAGGAGGAGGAG 851
703 GACCGGCTCTCTGACAGGAGCTGTGCGAGCCGCGCGGAGGAGGAGGAGGAGGCTC 762
852 CGGCTGCGGAGCTTCTCTGAGGAGTGTGCGGAGGAGGAGGAGGAGGAGGAGGAG 911
763 CCGAGCGGCTCTGAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 818
912 AAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 971
819 CTTCATATGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
972 CTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 10
US-10-684-206-37
Sequence 37, Application US/10684206
Publication No. US20050032725A1
GENERAL INFORMATION:
APPLICANT: Rao, Patricia
TITLE OF INVENTION: Molecules Associated with Regulatory T
FILE REFERENCE: TLN-021CP
CURRENT APPLICATION NUMBER: US/10/684,206
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/417102
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 60/417103
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 60/417243
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 60/419575
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US 60/424777
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 2395
TYPE: DNA
ORGANISM: Homo sapiens
US-10-684-206-37

Query Match 18.0%; Score 211; DB 19; Length 2395;
Best Local Similarity 59.4%; Pred. No. 3.1e-51;
Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

48 AGGCACTGGGGGATGAGTGGGGGCTCTTACAGACCGGCTCTCTGGGCAACCTGCT 107
217 AGGCGAAGCCAGCCATCAGCTCCGTCATGTTCTGCGCGGGGCTGCGGAACTCAT 276
108 GGGCTGGGGCTGCTGCGCGCTCGGGGCTGGGGT--GGTCTGCGGGCTCCACTGCGC 165
277 AGACTGGGCTGCTGCGCGCTGCGGGGACGTGGGGTGCAGCCCGCGCGAG 336
166 CCGCTGCC-CTGGCTCTTACATGCTGTGTGTGCTGACGGTCAACGACTTGTGGG 224
337 GAGCTCCCTCTCTTGTTCAGGTGTGTGAGCCGAGCTGTGTTCACCGACTGCTCGG 396
225 CAAGTCTCTTAAAGCCGGTGTGCTGCTTACGCTCAGAACCGAGTGTGCGGT 284
397 GACTCTCTTATCAGCCAGTGTGTACTGCTTCTGTACGCGCGGAAACCGCTGTGTC 456
285 GCTTGGCGCCGATGAGCACTGTTGTGCAAGCTTCCGCTTCTTCACTGCTTCTT 344
457 ACTGGGGCC-----GAGAGCGCGCGTGCACCTTCTGCTTCTGCACTGACTTCTT 510
345 TGGGCTCTCTGACACTGCACTCTGAGCATGAGCACTGAGTGTGCTCTCTCTAGG 404
511 GAGCTTGGCAGAGTCTCATGCTCTTTCGCAATGAGCCCTGAGGCGCTTCTCATGCG 570
405 GACCCCTTCTTCTTACAGAGGCACTTACACCTGCGCTGAGGCGCACTGTGAGCCCGCT 464
571 GACCCCTTCTTCTTACAGAGGCACTTACACCTGCGCTTCCGCGGCGCTGAGCGCTGCTGCT 630
465 GGTGAGCGCTTCTCTGCTGCTTCTGCGGCTTCTTCACTGAGGCTTGGGAACTTCT 524
631 CATCTATGAGTCTCTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
525 GAGTACTGCGCGGACCTGCTGCTTATTCAGATGTGTCCAGAGAGGAGCTGCTGCTGTC 584
691 CAGTACTGCGCGGAGCTGCTGCTTCAATCCGCAAGGAGGAGGAGGAGGAGGAGGAG 732
585 GGTGCTGGGGTACTGTGTCTCTACTTCACTGAGCTTCACTGAGGCTGCTGCTGCTGCTGCT 644

Db 541 GCTGGCGCTGATGATACCGTGTCTTCACTAATGCTTCTGCGCGGATATG 590

RESULT 7

US-10-029-386-23781
 ; Sequence 23781, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 ; FILE REFERENCE: AEOMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029, 386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 23781
 ; LENGTH: 371
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO CHR14.3
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
 ; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 7.00e-59
 ; OTHER INFORMATION: NT HIT: U31332.1, EVALUATE 0.00e+00
 ; OTHER INFORMATION: EST_HUMAN HIT: A1460323.1, EVALUATE 2.00e-16
 ; US-10-029-386-23781

Query Match 31.7%; Score 371; DB 16; Length 371;
 Best Local Similarity 100.0%; Pred. No. 9.2e-99;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 322 TTGCGCTTCTTCATGCTCTTCTTGGGCTCTCTCGACACTGCACTCTGCGCATGCGA 381
 Db 1 TTGCGCTTCTTCATGCTCTTCTTGGGCTCTCTCGACACTGCACTCTGCGCATGCGA 60
 Qy 382 CTGGAATGCTGCT 441
 Db 61 CTGGAATGCTGCT 120
 Qy 442 CTGGAATGCTGCT 501
 Db 121 CTGGAATGCTGCT 180
 Qy 502 TTGATGAGGCTTCTGGAAGTTCTGCAAGTCTGCGCGCGGCACTGCTGCTTATCCAGATG 561
 Db 181 TTGATGAGGCTTCTGGAAGTTCTGCAAGTCTGCGCGCGGCACTGCTGCTTATCCAGATG 240
 Qy 562 GTTCAAGAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
 Db 241 GTTCAAGAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 Qy 622 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
 Db 301 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 Qy 682 ATGACACCGGCG 692
 Db 361 ATGACACCGGCG 371

RESULT 8
 US-10-225-567A-286
 ; Sequence 286, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burner, Glenn C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 286
 LENGTH: 495
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-225-567A-286

Query Match 28.6%; Score 335; DB 15; Length 495;
 Best Local Similarity 82.7%; Pred. No. 4.3e-88;
 Matches 436; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

Qy 645 GCTGTGCAACTCTGCGCGCCATGCGCACTCTATGCGATGCAACCGCGCTGCAAGCGCA 704
 Db 1 GCTGTGCAACTCTGCGCGCCATGCGCACTCTATGCGATGCAACCGCGCTGCAAGCGCA 60
 Qy 705 CCGCGCTCTCTGACAGGAGCTGTGCGAGCGCGCGCGCGAGCGGAGGAGGAGCGCGCC 764
 Db 61 CCGCGCTCTCTGACAGGAGCTGTGCGAGCGCGCGCGCGAGCGGAGGAGGAGCGCGCC 120
 Qy 765 TGAGCCCTGAGAGAGCTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
 Db 121 TGAGCCCTGAGAGAGCTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Qy 825 TATGTTCTCTGCGCGCGATTTGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
 Db 181 TATGTTCTCTGCGCGCGATTTGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
 Qy 885 TAGGTGAGGCTTGAAGAAATTTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
 Db 203 -----TATGCGG 209
 Qy 945 CTTCATGAGAGCATTTAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
 Db 210 CTTCATGAGAGCATTTAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 269
 Qy 1005 ACCTCGAGCCTTGCAGTTCTATCTGATTTCAATTTGAGACCTTGGATTTTATCA 1064
 Db 270 ACCTCGAGCCTTGCAGTTCTATCTGATTTCAATTTGAGACCTTGGATTTTATCA 329
 Qy 1065 TTTTCAGATCTCAGATTTTTCGATTTTTCACAGATTTTTCACAGATTTTTCACAGATTTT 1124
 Db 330 TTTTCAGATCTCAGATTTTTCGATTTTTCACAGATTTTTCACAGATTTTTCACAGATTTT 389
 Qy 1125 ACAGAGCGGCTGAGCAATTTCACTAATGAGATTTCACTGATTTCACTGATTTCACTG 1171
 Db 390 ACAGAGCGGCTGAGCAATTTCACTAATGAGATTTCACTGATTTCACTGATTTCACTG 436

RESULT 9
 US-10-108-714-3
 ; Sequence 3, Application US/10108714
 ; Publication No. US20020128445A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Regan, John W.
 ; APPLICANT: Gil, Daniel W.
 ; APPLICANT: Woodward, David F.
 ; TITLE OF INVENTION: No. US20020128445A1 Human Prostaglandin EP Receptor
 ; FILE REFERENCE: 17023 DIV CIP
 ; CURRENT APPLICATION NUMBER: US/10/108,714
 ; CURRENT FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12

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; SEQ ID NO 24136
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL355833.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 1.00e-128
; OTHER INFORMATION: NT HIT: U13132.1, EVALUATE 0.00e+00
US-10-029-386-24136

Query Match      70.9%; Score 830; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 5.8e-234;
Matches 830; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CCGCTGCGCAACACACACCTCTGTGAAAAGGCACTCGGGGTATATGGGGGGTGTCT 77
DB 964 CCGCTGCGCAACACACACCTCTGTGAAAAGGCACTCGGGGTATATGGGGGGTGTCT 905
QY 78 CTTGACGACCGGCTCTCTGAGCAACCTGTGCTGAGCTGAGCTGAGCTGAGGCT 137
DB 904 CTTGACGACCGGCTCTCTGAGCAACCTGTGCTGAGCTGAGCTGAGGCT 845
QY 138 GGGGTGTGTCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
DB 844 GGGGTGTGTCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
QY 198 TGGCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
DB 784 TGGCTGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
QY 258 CTACGCTGACAAACCGAGTCTGCGGGTCTGCGCCGCACTTGAGCACTGCTGCTGCA 317
DB 724 CTACGCTGACAAACCGAGTCTGCGGGTCTGCGCCGCACTTGAGCACTGCTGCTGCA 665
QY 318 AGCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 377
DB 664 AGCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 605
QY 378 GGCACCTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTTCTTCTTCTTCTTCTTCT 437
DB 604 GGCACCTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTTCTTCTTCTTCTTCTTCT 545
QY 438 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
DB 544 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
QY 498 ACCTTTCATGAGCTTCTGGAAGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCT 557
DB 484 ACCTTTCATGAGCTTCTGGAAGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCT 425
QY 558 GATGTGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 424 GATGTGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 618 CATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
DB 364 CATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
QY 678 TGCATGACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
DB 304 TGCATGACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 738 GCGCGCGGACCGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
DB 244 GCGCGCGGACCGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 798 GGTGAGCTGATGACCGTGTCTTCTTCACTATGTTCTTCTGCGCGTAATTG 847
DB 184 GGTGAGCTGATGACCGTGTCTTCTTCACTATGTTCTTCTGCGCGTAATTG 135
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RESULT 6
US-10-029-386-10081
; Sequence 10081, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10081
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: U13132.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
US-10-029-386-10081

Query Match      50.4%; Score 590; DB 16; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.9e-163;
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CTACGCTGACAAACCGAGTCTGCGGGTCTTGGCGCCGCACTTGAGCACTGCTGCTGCA 317
DB 1 CTACGCTGACAAACCGAGTCTGCGGGTCTTGGCGCCGCACTTGAGCACTGCTGCTGCA 60
QY 318 AGCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 377
DB 61 AGCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
QY 378 GGCACCTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTTCTTCTTCTTCTTCTTCT 437
DB 121 GGCACCTGAGTGTGCTCTCTCTAGGCAACCTTCTTCTTCTTCTTCTTCTTCTTCT 180
QY 438 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
DB 181 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 498 ACCTTTCATGAGCTTCTGGAAGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCT 557
DB 241 ACCTTTCATGAGCTTCTGGAAGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCT 300
QY 558 GATGTGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 301 GATGTGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 618 CATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
DB 361 CATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 678 TGCATGACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
DB 421 TGCATGACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 738 GCGCGCGGACCGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
DB 481 GCGCGCGGACCGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 798 GGTGAGCTGATGACCGTGTCTTCTTCACTATGTTCTTCTGCGCGTAATTG 847
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Db	662	ACCGTGGGCTTTATTCAGATGCTCCAGAGGAGGAGCTCGCTGGGTGCTGGGTA	CT	721
Qy	601	GTGCTTA	CTCAGACCTCATGCGCTGCTGGTCTCTGGCACGTCGTGTGCAACTCTGGC	660
Ds	722	GTGCTTA	CTCAGACCTCATGCGCTGCTGGTCTCTGGCACGTCGTGTGCAACTCTGGC	781
Qy	661	GGCATGCGCAACCTCTATGCGATGACA	CCGGGCGCTGCGAGCGGCGACCCGCGCTCTGCAAC	720
Ds	782	GGCATGCGCAACCTCTATGCGATGACA	CCGGGCGCTGCGAGCGGCGACCCGCGCTCTGCAAC	841
Qy	721	AGGAGCTGTGCGGAGCGCGCGCGAG	CGGAGGAGAGGTCCTCCCTCAAGCCCTTGAGAG	780
Ds	842	AGGAGCTGTGCGGAGCGCGCGCGAG	CGGAGGAGAGGTCCTCCCTCAAGCCCTTGAGAG	901
Qy	781	CTGATCACTCTCTGCTGCTGCGCTG	ATGACCGTGTCTTTCACTATGTGTCTTGCC	840
Ds	902	CTGATCACTCTCTGCTGCTGCGCTG	ATGACCGTGTCTTTCACTATGTGTCTTGCC	961
Qy	841	GTAATGCAATTTGTTCCTGAGGTCC	CGGCGCAAGACCTGGAGTAAGTGAGGCTTGAG	900
Ds	962	GTAATTT-----	-----	967
Qy	901	AAACATTTTTCAGTCTGCTCTCTCT	CTCTTCTTCTCCAGATGCGCTTACTATGAGCAATT	960
Ds	968	-----	-----TATGCGCTTACTATGAGCAATT	990
Qy	961	TAAGAGATGTCAGAGAGAAAAACAG	AGACTCTTGAAAGAGCAGAGACACTCCGAGCTTGCG	1020
Ds	991	TAAGAGATGTCAGAGAGAAAAACAG	AGACTCTTGAAAGAGCAGAGACACTCCGAGCTTGCG	1050
Qy	1021	ATTTCATATCTGTGATTTCAATTGT	GGACCTTGAGATTTTATCATTTTTCAGATCTCGAT	1080
Ds	1051	ATTTCATATCTGTGATTTCAATTGT	GGACCTTGAGATTTTATCATTTTTCAGATCTCGAT	1110
Qy	1081	ATTTCGATATTTTTCACAAAGATT	TTTCATTAGACCTCTTAGTAGACAGAGCCGCTGACG	1140
Ds	1111	ATTTCGATATTTTTCACAAAGATT	TTTCATTAGACCTCTTAGTAGACAGAGCCGCTGACG	1170
Qy	1141	CAATTCACACTAACATGGAATCCAG	TCGTGTGA	1171
Ds	1171	CAATTCACACTAACATGGAATCCAG	TCGTGTGA	1201

RESULT 4
US-10-305-720-1474
; Sequence 1474, Application US/10305720
; Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhammer, Jeffrey J.
TITLE OR INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIORITY APPLICATION NUMBER: 09/016,434
PRIORITY FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1430
SOFTWARE: PERL Program
SEQ ID NO 1474
LENGTH: 1216
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 9940378
US-10-305-720-1474

Oy		6	GTAATGGAGCGGAGGCTCTTCAGACCGGCCTCTGGGAAACATGTGAGCCCTTGAGGACTG	120
Dd		410	GTGATGGAGCGGAGGAGTCTTTCAAGAACCGGCTCCTGGGACAACATGTGAGCCCTTGAGGACTG	469
Oy		121	CTGGCGGCGCTCGGAGGCTGAGGAGT	180
Dd		470	CTGGCGGCGCTCGGAGGCTGTGGAGT	529
Oy		181	TTCACATGT	240
Dd		530	TTCACATGT	589
Oy		241	CCGGT	300
Dd		590	CCGGT	649
Oy		301	GACACACTGTGTGTGCCAAGCCTTGCGCTTCTTCAATGTGTCTTGTGGGCTCTCTCGACA	360
Dd		650	GACACACTGTGTGTGCCAAGCCTTGCGCTTCTTCAATGTGTCTTGTGGGCTCTCTCGACA	709
Oy		361	CTGGAACCTCCGGGCGATAGGACATGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	420
Dd		710	CTGGAACCTCCGGGCGATAGGACATGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	769
Oy		421	CGACGGGACATCATCACCTGT	480
Dd		770	CGACGGGACATCATCACCTGT	829
Oy		481	CTGGCTTTTCTGCGGCGTACCTTTTATATGGGCTCTGGGAAATTCTGTGACAGTACTGTGCCGGC	540
Dd		830	CTGGCTTTTCTGCGGCGTACCTTTTATATGGGCTCTGGGAAATTCTGTGACAGTACTGTGCCGGC	889
Oy		541	ACCCTGATGACTTATTCAGATGATGATCCAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Dd		890	ACCCTGATGACTTATTCAGATGATGATCCAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGT	949
Oy		601	GTGCTTACTTCAGACCTTCATGAGCGCTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	660
Dd		950	GTGCTTACTTCAGACCTTCATGAGCGCTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1009
Oy		661	GCCATGTGGCAACCTCTATMGATGATGACACCGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGT	720
Dd		1010	GCCATGTGGCAACCTCTATMGATGATGACACCGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGT	1069
Oy		721	AGGAGACTGTGCGAGCGCGCGCGAGACGGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Dd		1070	AGGAGACTGTGCGAGCGCGCGCGAGACGGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1129
Oy		781	CTGATATCATCTCTGT	840
Dd		1130	CTGATATCATCTCTGT	1189
Oy		841	GTAATTG 847	
Dd		1190	GTAATTG 1196	

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RESULT 5
US-10-029-386-24136/C
; Sequence 24136, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEMOTICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

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Db      422 GACAACTGCTGGTCCAAAGCTTTCCTTCTTCAATGTCCTTCTTGGAGCTCTCCGACACA 481
Qy      361 CTGCAACTCTGGGCAATGGAATGGAATGCTGCTCTCCCTAGGAGCACTCTTCTTCTAC 420
Db      482 CTGCAACTCTGGGCAATGGAATGGAATGCTGCTCTCCCTAGGAGCACTCTTCTTCTAC 541
Qy      421 CGACGGCAATCAACCTCTGGGCTGAGGCACTGCTGAGCCCGGCTGCTGAGCCCTTCTCC 480
Db      542 CGACGGCAATCAACCTCTGGGCTGAGGCACTGCTGAGCCCGGCTGCTGAGCCCTTCTCC 601
Qy      481 CTGAGCTTTCGCGGCTACCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGTCTGCTCCCGG 540
Db      602 CTGAGCTTTCGCGGCTACCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGTCTGCTCCCG 661
Qy      541 ACCTGCTCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGGAGTTCGCTGAGGAGTTCGCT 600
Db      662 ACCTGCTCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGGAGTTCGCTGAGGAGTTCGCT 721
Qy      601 CTGCTCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGGAGTTCGCTGAGGAGTTCGCT 660
Db      722 CTGCTCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGGAGTTCGCTGAGGAGTTCGCT 781
Qy      661 GCCATGCGCAACCTTATGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 720
Db      782 GCCATGCGCAACCTTATGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 841
Qy      721 AGGAGCTGTCGCGAGCGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db      842 AGGAGCTGTCGCGAGCGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 901
Qy      781 CTGAGTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db      902 CTGAGTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
Qy      841 GTATATGCAATTTGTCTCTGAGTCCCGGCAAGACACTGAGGAGTAGGAGGAGGAGGAGGAG 900
Db      962 GTATAT----- 967
Qy      901 AAACATTTTCAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db      968 -----TATCGGCTTACTATGAGGAGT 990
Qy      961 TAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db      991 TAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
Qy      1021 ATTCTATCTGATTTTCAATTTGAGACCTTGGATTTTATCATTTTCAATTTTCAATTTT 1080
Db      1051 ATTCTATCTGATTTTCAATTTGAGACCTTGGATTTTATCATTTTCAATTTTCAATTTT 1110
Qy      1081 ATTCTATCTGATTTTCAATTTGAGACCTTGGATTTTATCATTTTCAATTTTCAATTTT 1140
Db      1111 ATTCTATCTGATTTTCAATTTGAGACCTTGGATTTTATCATTTTCAATTTTCAATTTT 1170
Qy      1141 CAATTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1171
Db      1171 CAATTCACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1201

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RESULT 3
US-10-128-558-263
; Sequence 263, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A

```

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; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PC_FU_genes Version 6.0
; SEQ ID NO 263
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-558-263

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Query Match 83.6%; Score 979; DB 18; Length 1253;
Best Local Similarity 92.2%; Pred. No. 7.3e-278;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

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Qy      1 ATGAATGCGCGCTTCTTACCGCTCCAGAAACCACTCTGTGAAAAGGCACTCGGCG 60
Db      122 ATGAATGCGCGCTTCTTACCGCTCCAGAAACCACTCTGTGAAAAGGCACTCGGCG 181
Qy      61 GTATGAGGCGGGGTGCTCTTACAGACCGGCTCTGAGGCAACTGCTGAGGCTGAGGCTG 120
Db      182 GTATGAGGCGGGGTGCTCTTACAGACCGGCTCTGAGGCAACTGCTGAGGCTGAGGCTG 241
Qy      121 CTGCGCGCTCTGCGGCGTGGGCTGCTGCGGCGTCACTGCGCGCTGCTGCGCTGCTGCT 180
Db      242 CTGCGCGCTCTGCGGCGTGGGCTGCTGCGGCGTCACTGCGCGCTGCTGCGCTGCTGCT 301
Qy      181 TTCTATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      302 TTCTATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
Qy      241 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db      362 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
Qy      301 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db      422 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
Qy      361 CTGCAACTCTGGGCAATGGAATGGAATGCTGCTCTCCCTAGGAGCACTCTTCTTCTAC 420
Db      482 CTGCAACTCTGGGCAATGGAATGGAATGCTGCTCTCCCTAGGAGCACTCTTCTTCTAC 541
Qy      421 CGACGGCAATCAACCTCTGGGCTGAGGCACTGCTGAGCCCGGCTGCTGAGCCCTTCTCC 480
Db      542 CGACGGCAATCAACCTCTGGGCTGAGGCACTGCTGAGCCCGGCTGCTGAGCCCTTCTCC 601
Qy      481 CTGAGCTTTCGCGGCTACCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGTCTGCTCCCGG 540
Db      602 CTGAGCTTTCGCGGCTACCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGTCTGCTCCCGG 661
Qy      541 ACCTGCTCTTTCATGAGGCTTTCGAGGAGTTCGCTGAGGAGTTCGCTGAGGAGTTCGCT 600

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PRIOR FILING DATE: 2000-02-28
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 412
 SOFTWARE: PL_FL_genes Version 6.0
 SEQ ID NO 24
 LENGTH: 1505
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (231) ..(1505)
 US-10-128-558-24

Query Match 84.8%; Score 992.8; DB 18; Length 1505;

Best Local Similarity 92.3%; Pred. No. 6,7e-282; Matches 1069; Conservative 0; Mismatches 57; Indels 32; Gaps 1;

1 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGGAAAAAGCAACTCGCGG 60
 231 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGGAAAAAGCAACTCGCGG 290
 61 GTGATGCGCGCGGCTCTTTCAGACCGCGCTCTGCGCAACTGCTGCGCTGCGCGCTG 120
 291 GTGATGCGCGCGGCTCTTTCAGACCGCGCTCTGCGCAACTGCTGCGCTGCGCGCTG 350
 121 CTGCGCGCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 180
 351 CTGCGCGCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 410
 181 TTCTACATGCTGCTGT 240
 411 TTCTACATGCTGCTGT 470
 241 CCGGT 300
 471 CCGGT 530
 301 GACAACTGCTGT 360
 531 GACAACTGCTGT 590
 361 CTGCAACTCTCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 591 CTGCAACTCTCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 650
 421 CGACGCGCATCATCCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 651 CGACGCGCATCATCCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 710
 481 CTGCGCTTCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 711 CTGCGCTTCTGCGCGCTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 770
 541 ACTGCTGTCTTATCTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 771 ACTGCTGTCTTATCTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 830
 601 GTGCTTCTTCTGAGCTGT 660
 831 GTGCTTCTTCTGAGCTGT 890
 661 GCGATGCGCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 891 GCGATGCGCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950
 721 AGGAGCTGTGCGAGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 951 AGGAGCTGTGCGAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
 781 CTGAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 1011 CTGAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070

841 GTAATTG-----CATTTGCTCGAGTCCCG 868
 1071 GTAAATTGAGTCCCCGGGGCCCCAGGCGAGCGAGGCACTGAGACTGTCCGGCGGGAGT 1130
 869 CCAGAGACCTGGAGAGTGTAGGCTTGAAGAAACATTTTCAGTGTCTCTCTCT 928
 1131 CCGGGCGGGAAGGTGTGAGCGGATCGGATGGACCGCGCGCGAGCGAGCTGCGCTG 1190
 929 TCTCCAGATATCGGCTTACTATGAGCACTTTAAGATGTCAAGAGAAACAGAGACC 988
 1191 GCCAGAGATATCGGCTTACTATGAGCACTTTAAGATGTCAAGAGAAACAGAGACC 1250
 989 TCTGAAGAAGCAGAGACCTCGAGCTTGCATTTTCTATCTGTATTTCAATTGAGAC 1048
 1251 TCTGAAGAAGCAGAGACCTCGAGCTTGCATTTTCTATCTGTATTTCAATTGAGAC 1310
 1311 CTTGGAATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1370
 1049 CTTGGAATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1108
 1371 ATTAGACCTTTAGCTAC 1126
 1372 ATTAGACCTTTAGCTAC 1388

RESULT 2

US-10-276-774-1020
 Sequence 1020, Application US/10276774
 Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 212/2-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 1020

LENGTH: 1253

TYPE: DNA

ORGANISM: Homo sapiens

Query Match 83.6%; Score 979; DB 17; Length 1253;

Best Local Similarity 92.2%; Pred. No. 7.3e-278; Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

1 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGAAAAAGCAACTCGCGG 60
 122 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGAAAAAGCAACTCGCGG 181
 61 GTGATGCGCGGCTCTTTCAGACCGCGCTCTGCGCAACTGCTGCGCGCTGCGCGCTG 120
 182 GTGATGCGCGGCTCTTTCAGACCGCGCTCTGCGCAACTGCTGCGCGCTGCGCGCTG 241
 121 CTGCGCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 180
 242 CTGCGCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 301
 181 TTCTACATGCTGCTGT 240
 302 TTCTACATGCTGCTGT 361
 241 CCGGT 300
 362 CCGGT 421
 301 GACAACTGCTGT 360

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 15:32:17 ; Search time 771.996 Seconds
(without alignments)
9208.852 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171

Sequence: 1 atgaagtcgcgcgtctaccg.....acatggatccagctctgga 1171

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 segs, 3035525691 residues

11267456

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09A_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length DB	ID	Description
1	992.8	84.8	1805	US-10-128-558-24	Sequence 24, Appl
2	979	83.6	1253	US-10-276-774-1020	Sequence 1020, Ap
3	979	83.6	1253	US-10-128-558-263	Sequence 263, App
4	847	72.3	1216	US-10-305-720-1474	Sequence 1474, App
5	830	70.9	964	US-10-029-386-24136	Sequence 24136, A
6	590	50.4	597	US-10-029-386-10081	Sequence 10081, A
7	371	31.7	371	US-10-029-386-23781	Sequence 23781, A
8	335	28.6	495	US-10-225-567A-286	Sequence 286, App
9	211	18.0	2396	US-10-108-714-3	Sequence 3, Appl
10	211	18.0	2395	US-10-684-206-37	Sequence 37, Appl
11	209.4	17.9	2372	US-10-225-567A-290	Sequence 290, App

12	209.4	17.9	2372	17	US-10-352-684A-35	Sequence 35, Appl
13	209.4	17.9	2372	17	US-10-366-286-35	Sequence 35, Appl
14	209.4	17.9	2372	17	US-10-305-720-1441	Sequence 1441, Ap
15	209.4	17.9	2372	18	US-10-755-889-91	Sequence 91, Appl
16	209.4	17.9	6446	17	US-10-139-686A-2	Sequence 2, Appl
17	208	17.5	501	16	US-10-029-386-10432	Sequence 10432, A
18	204.6	17.5	1077	16	US-09-825-509-558	Sequence 558, App
19	204.6	17.5	1077	19	US-10-925-095-558	Sequence 558, App
20	203.4	17.4	2824	17	US-10-108-260A-1464	Sequence 1464, Ap
21	201.8	17.2	1417	17	US-10-305-720-1403	Sequence 1403, Ap
22	201.8	17.2	1862	15	US-10-225-567A-284	Sequence 284, App
23	186.4	15.9	1242	18	US-10-349-528-3	Sequence 3, Appl
24	185	15.8	1360	9	US-09-917-800A-1482	Sequence 1482, Ap
25	108.8	9.3	1209	18	US-10-472-362-2	Sequence 2, Appl
26	108.8	9.3	1209	19	US-10-681-029-7	Sequence 7, Appl
27	108.8	9.3	3918	9	US-09-781-311-1	Sequence 1, Appl
28	107.2	9.2	1140	19	US-10-681-029-1	Sequence 1, Appl
29	107.2	9.2	1309	10	US-09-825-509-556	Sequence 556, App
30	107.2	9.2	1209	19	US-10-925-095-556	Sequence 556, App
31	107.2	9.2	1376	15	US-10-225-567A-288	Sequence 288, App
32	107.2	9.2	1376	17	US-10-305-720-1361	Sequence 1361, App
33	107.2	9.2	1376	18	US-10-473-974-179	Sequence 179, App
34	107.2	9.2	1473	14	US-10-243-501-1	Sequence 1, Appl
35	107.2	9.2	1473	14	US-10-243-501-2	Sequence 2, Appl
36	103.4	8.8	1473	14	US-10-243-351-1	Sequence 1, Appl
37	101.2	8.6	1467	10	US-09-826-509-560	Sequence 560, App
38	101.2	8.6	1467	19	US-10-925-095-560	Sequence 560, App
39	101.2	8.6	1554	15	US-10-320-351-1	Sequence 1, Appl
40	101.2	8.6	1554	15	US-10-320-351-2	Sequence 2, Appl
41	101.2	8.6	1958	15	US-10-225-567A-295	Sequence 295, App
42	101.2	8.6	1958	17	US-10-295-027-1109	Sequence 1109, App
43	101.2	8.6	1958	17	US-10-305-720-1380	Sequence 1380, App
44	101.2	8.6	1958	18	US-10-755-889-169	Sequence 169, App
45	101.2	8.6	1958	18	US-10-783-528-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-128-558-24
Sequence 24, Application US/10128558
Publication No. US20040219551A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Gezhi
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 812A
CURRENT APPLICATION NUMBER: US/10/128,558
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/339,453
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:55:17 ; Search time 4391.64 Seconds
(without alignments)
10149.570 Million cell updates/sec

Title: US-10-689-861-1
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	654	55.8	1053	5	BQ068035
3	554.4	47.3	3190	3	AK032488
4	393	33.6	495	7	CR747669
5	375.4	32.1	1996	3	AK016503
6	361.8	30.9	948	6	BY16183
7	333	28.4	486	1	AI460323
8	333	28.4	520	1	AA105532
9	313	26.7	632	2	BB622854
10	312	26.6	589	8	AZ291373
11	211	18.0	1077	9	AY410679
12	203.4	17.4	1038	3	BC017857
13	203.4	17.4	2020	3	CR601077
14	202.4	17.3	565	8	B2120059
15	192.6	16.4	1032	5	BM925026
16	188	16.1	652	5	BX498371
17	186.2	15.9	658	6	BY724253
18	185.6	15.8	765	1	AU132613
19	183.6	15.7	2509	3	AK086904
20	182.6	15.6	2653	3	AK036474
21	181.4	15.5	1077	9	AY410681
22	181.4	15.5	2619	3	AK054132
23	181.2	15.5	615	5	BP381970
24	176.4	15.1	571	8	AZ357037

25	170.6	14.6	1062	5	BM925058
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29	161.8	13.8	1019	1	AL552370
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32	150.2	12.8	562	6	CB609359
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35	139	11.9	771	4	BG919027
36	132	11.3	479	2	AW240093
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39	125.4	10.7	639	8	BH315818
40	125	10.7	482	5	BM986638
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42	121.6	10.4	653	7	CN484094
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ALIGNMENTS

RESULT 1
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LOCUS CD013871 Single gene library Homo sapiens cDNA, mRNA sequence.
DEFINITION CD013871.1 GI:37777401
ACCESSION CD013871
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1229)
Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Young, J. and Stuve, L.L.
PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
Genomics 83 (4), 566-571 (2004)
Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES

source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note=Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match: 97.6%; Score 1142.6; DB 6; Length 1229;
Best Local Similarity 99.5%; Pred. No. 6.1e-271; Indels 2; Gaps 2;
Matches 1167; Conservative 0; Mismatches 4;
QY 1 ATGAAGTCGCGGTTCTACCGTGCAGAACACCACTCTGTGGAAAAAGCAACTCGGCG 60
DB 4 ATGAAGTCGCGGTTCTACCGTGCAGAACACCACTCTGTGGAAAAAGCAACTCGGCG 63
QY 61 GTGATGGCGGGGTCTCTTTCAGACCGGCTCTCTGGGCAACCTCTGCGCCCTGGGGCTG 120

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Db 124 CTGGCGCGCTCGGGCTGGGGTGGTGTCTCGCGCGTCCACTGCGCGCGCTGCGCTCGGTC 183
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Qy 301 GACAACTGTTGTGGCAAGCCTTCGCTCTTCATGTCTCTTTGGGCTCTCTCTCGACA 360
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Qy 421 CGACGGCAATCACCTCGCTGCGCTGGCGCACTGGTGGCGCGGTGTGAGCGCTTCTCC 480
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Db 964 TAAAGATGTCAAGGAGAAAAACAGGACTCTGAAGAAGCAGAAGACCTCCGAGCCTTTC 1023
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RESULT 2

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BQ068035ACCESSION
BQ068035VERSION
BQ068035.1KEYWORDS
GI:19897081SOURCE
Homo sapiens (human)ORGANISM
Homo sapiensREFERENCE
1 (bases 1 to 1053)AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)JOURNAL
Unpublished (1999)COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLNL2829 row: 0 column: 09
High quality sequence stop: 645.

FEATURES

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1..1053

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5769056"

/lab_host="DH10B"

/clone_lib="NIH MGC 121"

/note="Torgan: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(in vitro). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 55.8%; Score 654; DB 5; Length 1053;

Best Local Similarity 96.0%; Pred. No. 2.5e-150; Indels 5; Gaps 4;

Matches 714; Conservative 0; Mismatches 25;

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Qy 61 GTGATGGCGGGGTCTCTTTCAGCAACCGGCTCTCTGGGCAACCTCTGCGCCCTGGGGCTG 120

Db 182 GTGATGGCGGGGTCTCTTTCAGCAACCGGCTCTCTGGGCAACCTCTGCGCCCTGGGGCTG 241

Qy 121 CTGGCGCGCTCGGGGTGGGTGTCTCGCGCGCTCCACTGCGCGCGCTGCGCCCTCGGTC 180

Db 242 CTGGCGCGCTCGGGGTGGGTGTCTCGCGCGCTCCACTGCGCGCGCTGCGCCCTCGGTC 301

Qy 181 TTCTACATGCTGTGTGGCTGTGAGCTGACCGCTTCTGCTGGGCAAGTGTCTCTTAAGC 240

Db 302 TTCTACATGCTGTGTGGCTGTGAGCTGACCGCTTCTGCTGGGCAAGTGTCTCTTAAGC 361

Qy 241 CCGGTGGTGTGGTGTGGCTGTGAGCTGAGAACCGGAGTGTGCGGGTGTGCGCCCGCATTTG 300

Db 362 CCGGTGGTGTGGTGTGGCTGTGAGCTGAGAACCGGAGTGTGCGGGTGTGCGCCCGCATTTG 421

Query Match		47.3%; Score 554.4; DB 3; Length 3190;
Best Local Similarity		71.1%; Pred. No. 1.3e-125;
Matches 829; Conservative		0; Mismatches 231; Indels 106; Gaps 3;
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QY	72	GGTGTCTTTCAGACCGGCTCTCGGCAACCTGTGGCCCTGGGCTGGGCGGCTC 131
DB	192	TGTGTCTTTCGGGTGGGGCTTCTGGGCAATCTTCTGGGCGCTGGTCTGGCGGCTC 251
QY	132	GGGGTGGGGTGGTGTCTCGCGCGCTCCACTGGCGCGGCTCGGCTCGCTTCTACATGCT 191
DB	252	GGGACTGGGGTCTTGGCGGCGAGGCCACTACACCGCGCGCTCGGCTTTTATGTGCT 311
QY	192	GGTGTGTGGCTGACGGTCAACGACTGTCTGGGCAAGTGCCTCTTAAGCCCGGTGGTGT 251
DB	312	CGTGTGTGGCTTACGGGTCAACGACTGTCTGGGCAATGTCTGTATCAGCCCGATGGTCT 371
QY	252	GGCTGCCTACGCTCAGAACCGAGTCTGGGGTGTCTGGCCCGCATTTGGACAACTCGT 311
DB	372	GGCTGCCTACGCGCAAAACAGAGCTAAAGAACTGTGCTGCTCAGGCAATCAGT 431
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DB	492	GGCTATGGCGGTGGAGTGTGTCTCTCTGGGACACCCCTTCTTCTACCAAGGCACT 551
QY	432	CACCTTGGCGCTGGGCGCACTGGTGGCCCGGTGTGAGCGCTTCTCCCTGGCTTTCTG 491
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QY	492	CGCGCTACCTTTTCATGGGCTTCGGGAAGTTCTGTGAGTACTCCCGCGGACCTGTGTCT 551
DB	612	TGGCTCCCTTGTGTGGTTTGGGAGTTCTGTGAGTACTGTCCAGGACCTGTGTGT 671
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QY	612	CAGCTCATGGCGTGTGTCTCTCGCACCGTGTGTGCACTCTCGGCGCATCGGCA 671
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DB	967	-----TATGTGCGTACTATGAGGCTTTAACTTG--- 997
QY	972	AGGAGAAACAGGACCTCTGAAGAGCAGAGACTCCGAGCCTTGGGATTTCTATCTG 1031
DB	998	-----AGAACAAAGCTGAAGAGACTCAGAGACCTCCAGCCTTGGCTTTCTCTGTG 1051
QY	1032	TGATTTCAATTGTGGACCTTGGATTTTATCAATTTTATCAGATCTCCAGTATTTCCGATAT 1091

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QY	1092	TTTTTCAAGATTTTTCATTAGACCTCTTAGGTACAGGCGCGGTGCAGCAATTC--- 1147
Db	1112	TATTTCAAGGTTTTCACAGACCTCTGATCTACAGAACTGGAGACCCATCCCCAGC 1171
QY	1148	--ACTAACATGGAATCCAGTCTGTGA 1171
Db	1172	AAAGTAACTGGATCCACTTTGTGA 1197

CR747669

495 bp mRNA linear EST 30-AUG-2004

CR747669 NIH_MGC_121 Homo sapiens cDNA clone IMAGE99800912829 ;

IMAGE:5769056 5', mRNA sequence.

CR747669

CR747669.1 GI:51661368

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 495)

Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., Peters, M., Radelof, U. and Schneider, D.

I.M.A.G.E. cDNA Clone Collection

Unpublished (2004)

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

RZPD; IMAGE99800912829.

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACAGCAACAGCTATGAC.

Location/Qualifiers

1..495

/organism="Homo sapiens"

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/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 33.6%; Score 393; DB 7; Length 495;

Best Local Similarity 100.0%; Pred. No. 5.9e-86;

Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	103	ATGAGTCCGCTTCTACCGTCCAGAACACCACTCTGTGAAAAAGGCAACTCGGGC 162
QY	61	GTGATGGCGGGGTGCTCTTCAGCACCGGCTCTCTGGGCAACCTGCTGCGCCCTGGGGCTG 120


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QY 132 GGGGCTGGGGTGGTGTCTCGCGGGCTCCACTGGCGCCCGCTGCCCTCGGTCTTCTTACATGCT 191
D 460 GGGACTGGGGTCTTGGCGGCCAGGGGCACTACACCGCGCGCTCGGTCTTTTATGTGCT 401
QY 192 GGTGTGTGGCTTGGCTGACCGGCTTGGCGGAGTGGTGGCGAGTGGCTTAAAGCCGGTGGTGT 251
D 400 CGTGTGTGGCTTGGCGGCTTGGCGGAGTGGTGGCGAGTGGTGGCGAGTGGTGGCGAGTGGTGT 341
QY 252 GGCTGCTACGCTCAGAACCGGAGTCTGGGGGTGGTCTGGCGCCGCAATTGGCAAACTCGTT 311
D 340 GGCTGCTACGCTCAGAACCGGAGTCTGGGGGTGGTCTGGCGCCGCAATTGGCAAACTCGTT 281
QY 312 GTGCCAAGCTTGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 371
D 280 ATGCCAAAGCTTGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 221
QY 372 GGCCTAGGCTTGGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 431
D 220 GGCCTAGGCTTGGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 161
QY 432 CACCTTGGCTTGGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 491
D 160 CACCTTGGCTTGGGCTTCTTATGTCCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCTTGGGCTTCT 101
QY 492 CGCGTACCTTTCATGGCTTGGGAGTTCGTGCAAGTTCGTGCAAGTTCGTGCAAGTTCGTGCAAGTTC 551
D 100 TCGCTTCCCTTTCATGGCTTGGGAGTTCGTGCAAGTTCGTGCAAGTTCGTGCAAGTTCGTGCAAGTTC 41
QY 552 TATCCAGATGGTCCACGAGGGCTTGGTTCGGTG 588
D 40 CATCCAGATGGTCCACGAGGGCTTGGTTCGGTG 4

```

RESULT 7

```

LOCUS AI460323/c 486 bp mRNA linear EST 09-MAR-1999
DEFINITION ao95a01.x1 Schiller meningioma Homo sapiens cDNA clone
IMAGE:1953576 3' similar to SW:PD2R_HUMAN Q13258 PROTAGLANDIN D2
RECEPTOR 1, mRNA sequence.

```

```

ACCESSION AI460323
VERSION AI460323.1 GI:4313204
KEYWORDS EST.
SOURCE Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE 1 (bases 1 to 486)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krisman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.

```

```

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

```

```

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1953576"
/sex="female"
/tissue_type="meningioma"

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```

FEATURES source

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/dev_stage="72 years"
/lab_host="SOUR"
/clone_lib="Schiller meningioma"

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```

Note="Organ: brain; Vector: pBluescript SK- (Stratagene);
Site 1: EcoRI; Site 2: XhoI; Double-stranded cDNA was
prepared from human_meningioma using primer
5'-GAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. Tumor
identification by consensus pathology. This library was
constructed by Dr. Martin Schiller (Johns Hopkins
University)."
```

ORIGIN

```

Query Match 28.4%; Score 333; DB 1; Length 486;
Best Local Similarity 82.7%; Pred. No. 3.8e-71;
Matches 434; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 647 TGTGCAACCTCGGCGCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGGCACC 706
D 486 TGTGCAACCTCGGCGCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGGCACC 427
QY 707 CGCGTCTCTGCACGAGGACTGTGCGAGCGCGCGGAGCGGAGGAGGAGGCTGCCCTC 766
D 426 CGCGTCTCTGCACGAGGACTGTGCGAGCGCGCGGAGCGGAGGAGGAGGAGGCTGCCCTC 367
QY 767 AGCCCTCGGAGGAGTGGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 826
D 366 AGCCCTCGGAGGAGTGGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
QY 827 TGTGTTCTCTGCGCCGTAATTGTCATTTGTTCTCGGAGTCCCGCCCAAGACACCTGGGAGTA 886
D 306 TGTGTTCTCTGCGCCGTAATTGTCATTTGTTCTCGGAGTCCCGCCCAAGACACCTGGGAGTA 287
QY 887 GGTGAGGCTTGAGGAAACATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 946
D 286 -----TATCGCGCT 278
QY 947 TACTATGGAGCATTTAAGGATGTCAGGAGAGAAACAGGACCTCTGAAGAACAGAGAC 1006
D 277 TACTATGGAGCATTTAAGGATGTCAGGAGAGAAACAGGACCTCTGAAGAACAGAGAC 218
QY 1007 CTCGAGGCTTGGCATTTCTATCTGATGTTTCAATTGTTGGACCTTGGATTTTATCAT 1066
D 217 CTCGAGGCTTGGCATTTCTATCTGATGTTTCAATTGTTGGACCTTGGATTTTATCAT 158
QY 1067 TTCAGATCTCCAGTATTCGAGATATTTTTCACAGATTTTTCATTTAGACCTCTTAGGTAC 1126
D 157 TTCAGATCTCCAGTATTCGAGATATTTTTCACAGATTTTTCATTTAGACCTCTTAGGTAC 98
QY 1127 AGGAGCGGTCGCGCAATTCCACTAACATGGAATCCAGTCTGTGA 1171
D 97 AGGAGCGGTCGCGCAATTCCACTAACATGGAATCCAGTCTGTGA 53

```

RESULT 8

```

LOCUS AA105532 520 bp mRNA linear EST 30-OCT-1996
DEFINITION mos7a09.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
clone IMAGE:557656 5' similar to TR:G57719 G57719 PROTAGLANDIN D
RECEPTOR 1, mRNA sequence.
ACCESSION AA105532
VERSION AA105532.1 GI:1654672
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 520)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

```

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE JOURNAL COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:338448

Seq primer: -28M13 rev1 from Amersham

High quality sequence scop: 475.

FEATURES source

Location/Qualifiers
1..520
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:557656"
/tissue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site: 1;
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 8.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN

Query Match 28.4%; Score 333; DB 1; Length 520;
Best Local Similarity 78.7%; Pred. No. 3.9e-71;
Matches 410; Conservative 0; Mismatches 110; Indels 1; Gaps 1;
QY 40 GTGGAAAGGCAACTCGCGGTGTATGGCGGGGTCTTTCAGCACCGGCTCTCTGGGC 99
DB 1 GTGGAAAGGGGTCTCTCGCGAGATGGCGGTGTCTCTCGTGGGGGTCTCTGGGC 60
QY 100 AACCTGTGGCCCTGGGGCTGTGGCGGCTCGGGCTGGGGTGTGTCTCGCGGGGTGCA 159
DB 61 AATCTTCTGGCGCTGTGTCTGTGGCGGCTCGGACTGGGGTCTTTCGGCGCAGGCA 120
QY 160 CTGGCGCGCTGCCCTCGGTCTTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 219
DB 121 CTACACCGCGCGCTCGGTCTTTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 220 CTGGGCAAGTGTCTTAAAGCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 279
DB 181 CTGGGCAAGT 240
QY 280 CGGGTGTGTGGCCCGCAATGGACAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 339
DB 241 AAGGAACTGTGCTGCTGCTCAG-GAATCAGTTATGCGAAACGTTGCGCTTCTGTATGCC 299
QY 340 TTCTTTGGGCTCTCTCGACATGCAATCTCTGGCCATGGCACTGGAGTGTGTGTGTGTGT 399
DB 300 TTCTTTGGGCTAGCTCGACCTTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 359
QY 400 CTAGGCAACCTTTCTTCTTACAGCGGCACATCCTCTGGCCATGGCACTGGAGTGTGTGT 459
DB 360 CTGGGACACCTTTCTTCTTACAAAGGACATGCTGTGTGTGTGTGTGTGTGTGTGTGT 419
QY 460 CGGGTGTGTGGCGGCTTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 519
DB 420 CGGGTGTGTGGCGGCTTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 479
QY 520 TTCTGTGAGTACTGCGCGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 560
DB 480 TTCTGTGAGTACTGCGCGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 520

RESULT 9 BB622854

LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BB622854 632 bp mRNA linear EST 26-OCT-2001
BB622854 RIKEN full-length enriched, adult male olfactory brain Mus
musculus cDNA clone 6430566C09 5', mRNA sequence.

BB622854
EST
BB622854.1 GI:16461752

Mus musculus (house mouse)

Mus musculus

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahira, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

1..632

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="6430566C09"

/sex="male"

/tissue_type="olfactory brain"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, adult male

olfactory brain"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN, Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCGCAACTCTGTGGAAAAGGCAACTCGCGGATGGCGG 71 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGATTAAATTAATCCCGCCCGCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

ORIGIN

Query Match 26.7%; Score 313; DB 2; Length 632;
Best Local Similarity 76.2%; Pred. No. 3.5e-66;
Matches 385; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 12 GTTCTACCGCTGCCAGAACCACTCTGTGGAAAAGGCAACTCGCGGATGGCGG 71
DB 128 GTCTATCTCTGTACACATCCACCTGGGTGGAAAGGGCTCTCTCGCGACGATGGCGC 187
QY 72 GGTGTCTTTACGACCGGCTCTCTGGCAACCTGTGGCCCTGGGGCTCTGGCGGCTC 131
DB 188 TGTGTCTTTGGTGGGGCTCTCTGGCAATCTTCTGGCGCTGGTCTCTGGCGGCTC 247
QY 132 GGGGCTGGGGTGGTGTCTCGCGGCTCCACTGGCGCGCGCTCGCCCTCGGTCTTCTACATGCT 191
DB 248 GGGACTGGGGTCTTGGCGGCGGCGCACTACACCGCGCGCTCGGTCTTCTATGTGCT 307
QY 192 GGTGTGTGCGCTGACGGTCAACGCTTGTGGCAAGTCCCTTAAGCCCGGTGGTGT 251
DB 308 CGTGTGTGCTTGACGGTCAACGCTTGTGGCAATCTCTGATCAGCCCGATGCTCT 367
QY 252 GGTCTGCTACGCTCAGAACCGGAGTCTGGGGTGTCTGGCGCGGCTTGGCAACTCGT 311
DB 368 GGTCTGCTACGCGCAAAACAGAGCCTAAGGAACCTGTGGCTCGCTCAGGCAATCAGT 427
QY 312 GTGCCAAGCTTCGCGCTTCTTATGTCCTTCTTGGGCTCTCTCGACACTGCAACTCT 371
DB 428 ATGCGAAGCTTCGCGCTTCTTATGTCCTTCTTGGGCTAGCTCGACCTTACAGTGT 487
QY 372 GGGCATGACCTGGAGTGTGGCTTCCCTAGGGACCTTCTTCTTCTACCGAGGCAAT 431
DB 488 GGTATGCGGCTGGAGTGTGGCTTCTCTGGACACACCTTCTTCTACCAAAAGCAGT 547
QY 432 CACCTTGGCGCTGGCGCACTGGTGGCGCGGCTGGTGGAGGCTTCTCTCGCTTCTG 491
DB 548 CACCTTGGCGCGGAGTGTGGTGGACACCGGCTGGGGGCGGCTTCTGCTTGGCTTCTG 607
QY 492 CGCGGTACCTTTTCATGGGCTTCGGG 516
DB 608 TGGGCTCCCTTGTGGTTTGGG 632

RESULT 10

AZ291373/c
LOCUS 589 bp DNA linear GSS 27-JUL-2000
DEFINITION RPI-23-131N24.TV RPI-23 Mus musculus genomic clone
RPI-23-131N24, genomic survey sequence.

ACCESSION

AZ291373

VERSION

AZ291373.1 GI:9533213

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 589)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatman, S.,

Akinret, B., Levins, M., McGann, S., Tsagaye, G., Geer, K., Krol, M., de

Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPI-23

Unpublished (1999)

COMMENT

Other_GSSs: RPI-23-131N24.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org
Clones are derived from the mouse BAC library RPI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_end/mouse/bac_end_intro.html
Plate: 131 row: N column: 24
Seq primer: T7
Class: BAC ends.

FEATURES

source

1..589
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-23-131N24"
/sex="female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1: EcorI; Site 2: EcorI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcorI and EcorI Methyase. Size selected DNA was cloned into the pBACE3.6 vector at the EcorI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 26.6%; Score 312; DB 8; Length 589;
Best Local Similarity 78.8%; Pred. No. 6.1e-66;
Matches 372; Conservative 100; Mismatches 100; Indels 0; Gaps 0;

QY 376 ATGGCACTGGAGTGTGGCTCTCCCTAGGGGACCTTCTTCTACCGCGGACATCACC 435
DB 588 ATGGCGGTGAAGTGTGGCTGTCTTGGCACACCTTCTTACAAAGGACGTCACC 529
QY 436 CTGGCCCTTGGGCGCACTGGTGGCCCGGTGGTGGAGCGCTTCTCCCTGGCTTCTCGCGG 495
DB 528 TTGCGCCGGGAGTGTGGTGGCACCGGTGGTGGCGGCTTCTGTGGCTTCTGTGGG 469
QY 496 CTACCTTTTCATGGGCTTCGGGAAGTTGTGCAAGTACTGCCCCGGCACCTGGTGTCTTATC 555
DB 468 CTCCCTTTTGTGGTTTGGGAAGTTCTGTGCAAGTACTGTCCAGGACCTGTGTTCATC 409
QY 556 CAGATGGTCCAGGAGGGCTGGTGTGGTGTGGGCTACTGTGTCTTACTCCAGC 615
DB 408 CAGATGATCCAGAGGCGTTCATTTTCGGTAATAGGCTTCTGTGTCTTACTCCAGC 349
QY 616 CTCATGGCGCTGTGGTCTCTCGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
DB 348 CTCATGGCGCTGTGGTCTCTCGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 289
QY 676 TATGCGATGCACCGCGGCTGCAGCGGACCCCGGCTCTGTGCACAGGAGTGTGCCGAG 735
DB 288 TATGACATGCACAGCGCGCCAGAGGCACTATCTCACCGCTGTCTCCAGGACCGGCCAG 229
QY 736 CGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 795
DB 228 TCAGGCTCAGACTACAGGACCGGGTCCCTGTGATCTCTTTGGAGGAGCTGGACCATATG 169
QY 796 CTGCTGGCGCTGTACCGCTGTCTTCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
DB 168 CTGCTGGCTCTCATACAGTGTCTTTCACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 117

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 36 Row: 1 Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506262
This clone has the following problem: retained intron.

FEATURES
source
1..1038
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/db_xref="taxon:9606"
/clone="IMAGE:4690793"
/tissue_type="Lung"
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/lab_host="DH10B"
/note="Vector: pDNR-LIB"

ORIGIN
Query Match 17.4%; Score 203.4; DB 3; Length 1038;
Best Local Similarity 61.6%; Pred. No. 4.5e-39; Indels 12; Gaps 3;
Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;

QY 98 GCAACCTGTCGGGCTGCTGGCGGCTGCTGGGGCTGGGGTGGTCTCGCGCGTC 157
DB 112 GCACCTGATGTTCTGGCGGCTGGTGGGCAACGGGCTGGCCCTGGGCATCCTGAGCG 171

QY 158 CACTGCGCC---CGTGGCCCTGGTCTTACATGCTGTGTGTGGCTGAGCGTCAACGG 214
DB 172 CACGGCGACCGCGCGCCCTCGGCTTGGCGTGTGGTGGCGACTGGCGGCCACCG 231

QY 215 ACTTGTGGGCAAGTCCCTTAAGCCGGTGGTGGCTGCTGCTGCTGCTGAGTACGACCGGA 274
DB 232 ACTGTGGGCAACGACTTCTGAGCCCGCGGCTGTCTGGCCCTATGCGCGCAACAGCT 291

QY 275 GTCTGGGCTGCTGGCGCCCGCATTTGGCAACTCTGTTGTGGCAAGCTTTCGCTTCTCA 334
DB 292 CCTGTGGGCT---GGCCGAGGCGGCCCGCCCTGTGCGATGCTTGGCTTGGCCA 348

QY 335 TGTCTCTTTTGGGCTCTCTCGACACTGCAACTCTGTGGCCATGGCACTGGAGTGTGTCG 394
DB 349 TGACCTTCTTGGGCTGGGCTCATGCTCATCTCTTTGGCCATGGCGGTGGAGCGTGGC 408

QY 395 TCTCCCTAGGCAACCTTCTTCTACGAGCGACATCACCTTGGCCCTGGGGGCACTGG 454
DB 409 TGGCGCTGAGCCACCCCTACCTCTAGCGCAGCTGGACGGGCGCCGCTGCGCCCGCTGG 468

QY 455 TGGCCCGGCTGGTGGAGCGCTTCTCCCTGGCTTCTGCGCGCTACCTTTCATGGGCTTCG 514
DB 469 CGCTGCCACCATCTAGGCTTCTGGTCTCTTCTGGCGGCTGCCCCCTGTGGGCTGG 528

QY 515 GGAAGTTCGTGAGTACTCCCGCGCACTGTGTCTTATTCAGATGTGTCCACGAGAGG 574
DB 529 GCCAACACACGAGTACTGCCCGCGCAGCTGGTGTCTTCTCGGCATGCGC-----TGGG 582

QY 575 GCTCGCTGCGTGGGGTACTCTGTGCTCTACTCCAGCCTCATGGGCTGCTGCTTC 634
DB 583 CCCAGCGGGCGCGCGCTTCTGCTGGCCCTAGCGCGGCTGGTGGGCTGCTGCTGCTG 642

QY 635 TCGCCACCGTGTGTGCAACCTCGGCGCAATGCGCAACCTCTATGCGATGACCGCGCGC 694
DB 643 CTGGCATCTTCTTGTGCAAGGCTGGTCACTTACCTTACGCTCTGCGGCATGTACCGCAGC 702

QY 695 TGCAGGGGACCGCGGCTC 713
DB 703 AGAAGGGCCACCGGCTC 721

RESULT 13
LOCUS CR601077 2020 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI069YD07 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION CR601077
VERSION CR601077.1 GI:50481884
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2020)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue
2 (bases 1 to 2020)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source
1..2020
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN
Query Match 17.4%; Score 203.4; DB 3; Length 2020;
Best Local Similarity 61.6%; Pred. No. 5.2e-39; Indels 12; Gaps 3;
Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;

QY 98 GCAACCTGTCGGGCTGCTGGCGGCTGCTGGGGCTGGGGTGGTCTCGCGCGTC 157
DB 135 GCACCTGATGTTCTGGCGGCTGGTGGGCAACGGGCTGGCCCTGGGCATCCTGAGCG 194

QY 158 CACTGCGCC---CGTGGCCCTGGTCTTACATGCTGTGTGGCTGAGCGTCAACCG 214
DB 195 CACGGCGACCGCGCGCCCTTCGGCTTTCGGCGGTGCTGGTACCGGACTGGCGGCCACCG 254

QY 215 ACTTCTGGGCAAGTCCCTTAAGCCGGTGGTGGCTGCTGCTGCTGCTACGCTACGACCGGA 274
DB 255 ACCTGCTGGGCAACGACTTCTGAGCCCGCGGCTGTCTGTGGCTATGCGCGCAACAGCT 314

QY 275 GTCTGGGCTGTCGGGCGCGCATTTGGACAACCTGTTGTGGCAAGCTTTCGCTTCTTCA 334
DB 315 CCCTGCTGGGCT---GGCCCGAGCGCGCCCGCTGTGCGCATGCTTTCGCTTTCGCCA 371

QY 335 TGTCTCTTTTGGGCTCTCTCGACACTCTGCGCACTCTGCGCCATGCACTGGAGTCTGCG 394
DB 372 TGACCTTCTTGGGCTGGCGTCCATGCTCTCTTTTGGCATGGCCGTGGAGCGCTGCG 431

QY 395 TCTCCCTAGGCGACCGCTTCTTCTACCGAGCGCACATCACCTTGGCGCTGGCGCGACTGG 454
DB 432 TGGCGCTAGGCACCCCTACCTCTACGCGCAGCTGGAACGGGCGCGCTGCGCCCGCTGG 491


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/clone="IMAGE:5762304"  
/lab_host="DH10B"  
/clone_lib="NIH_MGC_122"  
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH_MGC Library."
```

ORIGIN

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Query Match 16.4%; Score 192.6; DB 5; Length 1032;  
Best Local Similarity 60.4%; Pred. No. 2.1e-36;  
Matches 374; Conservative 0; Mismatches 234; Indels 11; Gaps 3;  
  
QY 98 GNAACCTGCTGGCCCTGGGGCTGCTGGCGGCTCGGGGCTGGGGTGGTGTGCTGGCGGCTC 157  
DB 142 GCACCTGATGTTCTGGCGGGTGGTGGGCAACGGGCTGGCCCTGGGCATCCTGAGCG 201  
  
QY 158 CACTGCGCC---CGCTGCCCTCGGTCTTCTACATGCTGTGTGTGGCTGACGGTCACCG 214  
DB 202 CACGGCGACCGGCGGCCCTCGGCCCTTCGGGTGCTGTGCTACCGGACTGGCGGCCACCG 261  
  
QY 215 ACTTGCTGGGCAAGTGCCTCAAGCCGGTGGTGTGCTGCTACGCTCAGAACCGGA 274  
DB 262 ACTGCTGGGCAACAGCTTCTCTAGGCCCGGCGGTGTTCTGGGCTATGGCGCAACAGCT 321  
  
QY 275 GTCTGGGGTGTGTCGGCCGCAATTGGACAACCTGTTGTGCCAAGCCTTCGCCCTTCTTCA 334  
DB 322 CCTGCTGGGCT---GGCCCGAGGGGCGCCGCCCTGTGCGATGCTTGGCTTGGCTTGGCCA 378  
  
QY 335 TGTCTCTTCTTTGGGCTCTCTCGACACTGCAACTCTGGCCCATGGCACTGGAGTGGTGGC 394  
DB 379 TGACCTTCTTGGGCTGGCGTCCATGCTCATCTCTTTGCCATGGCCGTGGAGCGCTGCC 438  
  
QY 395 TCTCCTTAGGGCACCTTCTTCTACCGGCGACATCACCTCGCCCTGGGCGCACTGG 454  
DB 439 TGGCGGTGAGCCACCCCTACCTCTAGCGGAGTGGACGGGGCCCGCTGGCGCCGCTGG 498  
  
QY 455 TGGCCCCGGTGGAGCGCTTCTCCCTGGCTTTCTGGCGGTACCTTTTCAATGGGCTTCG 514  
DB 499 CGCTGCCAGCCATCTACGCGCTTCTGGCTCTCTTCTGGCGGCTGCCCTGCTGGGCTGG 558  
  
QY 515 GGAAGTTCTGAGTACTGCCCCGGGACCTGGTGTCTTATCCAGATGGTCCACGAGGAGG 574  
DB 559 GCCAACACAGCAGTACTGCCCGGCGAGCTGGTGTCTCTCCGCAATG-----CGCTGGGC 613  
  
QY 575 GCTCGCTGTGGTGGGTACTCTGTCTCTACTCCAGCCTCATGGCGCTGCTGGTCC 634  
DB 614 CCAGCGGGGGGCGCGCCCTTCTCGGTGGCTACGCCGGCCCTGGTGGGCTGCTGGTGG 673  
  
QY 635 TGGCCACCGTGTGTGCAACCTGGCGGCGCATGGCAACCTCTATGCGATGCAACCGCGGC 694  
DB 674 CTGGCATCTTCTCTGCAAGGCTGGTCACTCCCTCAGCCTCTGCTGCTATGACCGCAGC 733  
  
QY 695 TGCAGCGGACCGCGCTC 713  
DB 734 AGAAGCGCCACCGGCTC 752
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Search completed: April 22, 2005, 17:52:57
Job time : 4397.64 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 17:53:08 ; Search time 54.229 Seconds
(without alignments)

2111.067 Million cell updates/sec

Title: US-10-689-861-2

Perfect score: 1541

Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVGVPKTPGSR 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1467	95.2	359	2	Aaw03516 Prostagla
2	1467	95.2	359	4	Aam79009 Human pro
3	1467	95.2	359	6	Abp81901 Human pro
4	1467	95.2	359	7	Ad448182 Human pro
5	1467	95.2	359	8	Ado29614 Human GPC
6	1467	95.2	369	3	Aay94346 Human cel
7	1467	95.2	399	4	Abb12000 Human pro
8	1467	95.2	399	4	Aam79993 Human pro
9	1467	95.2	399	7	Ado90940 Novel pro
10	1467	95.2	424	7	Ade07993 Novel pro
11	1125	73.0	357	7	Ad448180 Rat Prote
12	1100	71.4	357	8	Ado29615 Mouse GPC
13	1099	71.3	357	2	Aar84708 Prostagla
14	595.5	38.6	362	8	Ado29619 Mouse GPC
15	586	38.0	358	6	Abp81903 Human pro
16	586	38.0	358	7	Ad448180 Human pro
17	586	38.0	358	7	Adx52578 Hematolog
18	586	38.0	358	8	Ado29618 Human GPC
19	586	38.0	358	8	Adri4091 Human NF-
20	586	38.0	358	8	Adri4385 Prostagla
21	586	38.0	609	2	Aay41279 Fusion pr
22	585	38.0	358	2	Aaw44246 Human HP4
23	585	38.0	358	5	Abg30499 Human HP4
24	585	38.0	358	8	Ado05738 Human pro
25	580	37.6	358	4	Abb56383 Non-endog

ALIGNMENTS

RESULT 1
AAW03516
ID AAW03516 standard; protein; 359 AA.

XX	AC	AAW03516;			
XX	DT	11-MAR-1997 (first entry)			
XX	DE	Prostaglandin DP receptor.			
XX	KW	Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;			
XX	KW	smooth muscle; nervous tissue; G protein-coupled receptor; modulator;			
XX	KW	mouse; prostaglandin-related disease; therapy.			
XX	OS	Homo sapiens.			
XX	PN	WO9623066-A2.			
XX	PD	01-AUG-1996.			
XX	PF	23-JAN-1996; 96WO-CA0000047.			
XX	PR	26-JAN-1995; 95US-00378682.			
XX	PA	(MERI) MERCK FROSST CANADA INC.			
XX	PI	Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;			
XX	DR	WPI, 1996-362690/36.			
XX	DR	N-PSDB; AAT37402.			
XX	PT	Human prostaglandin DP receptor and related DNA - used to identify			
XX	PT	receptor modulators to treat prostaglandin-related diseases.			
XX	PS	Claim 2; Page 41; 49pp; English.			
XX	CC	This sequence represents the human prostaglandin DP receptor. The DP			
XX	CC	receptor is the least ubiquitous and least abundant of the prostanoid			
XX	CC	receptors. The DP receptors are thought to be distributed mainly in blood			
XX	CC	platelets, smooth muscle of various tissues, and nervous tissue			
XX	CC	(including the central nervous system). However, many of the actions and			
XX	CC	distribution of the DP receptor is species dependent. This receptor is a			
XX	CC	G protein-coupled receptor which can specifically bind prostaglandin			
XX	CC	molecules. The DNA encoding this sequence was isolated using primers (see			
XX	CC	AAT37403 and AAT37404) based on the N-terminal sequence, and an internal			
XX	CC	sequence from purified mouse DP. The human prostaglandin DP receptor can			
XX	CC	be used to identify modulators of the receptor. The identified modulators			
XX	CC	can then be used to treat prostaglandin-related diseases, and for			

26	564	36.6	358	2	AAW08135	Aaw08135 Human cyt
27	564	36.6	358	3	AAy87954	Aay87954 Human CR3
28	519	33.7	415	8	ADO29627	Ado29627 Mouse GPC
29	518.5	33.6	284	8	ADQ95982	Adq95982 T cell ac
30	518.5	33.6	289	7	ADM05222	Adm05222 Human pro
31	518.5	33.6	296	8	ADQ95984	Adq95984 T cell ac
32	518.5	33.6	386	2	AAR81979	Aar81979 Human pro
33	518.5	33.6	386	2	AAR81980	Aar81980 Human pro
34	518.5	33.6	386	6	ABP81900	Abp81900 Human pro
35	518.5	33.6	386	7	ADP03580	Adp03580 Human GPC
36	518.5	33.6	386	8	ADO29626	Ado29626 Human GPC
37	518.5	33.6	386	8	ADQ95940	Adq95940 T cell ac
38	516	33.5	253	8	ADP29755	Adp29755 Human sec
39	513.5	33.3	386	2	AAR74915	Aar74915 Prostagla
40	506.5	32.9	416	2	AAR81981	Aar81981 Rat prost
41	432	28.0	414	7	ADP03569	Adp03569 Human GPC
42	389	25.2	513	2	AAR42282	Aar42282 PGE2 rece
43	389	25.2	513	8	ADO29623	Ado29623 Mouse GPC
44	364.5	23.7	480	8	ADR46683	Adr46683 Cancer-as
45	364.5	23.7	488	2	AAW02271	Aaw02271 Human pro

```
CC modulating the effects of prostaglandins on the DP receptor
XX
SQ Sequence 359 AA;
Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPYRCQNTTSVEKGNQAVMGVLFSTGLGNLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPYRCQNTTSVEKGNQAVMGVLFSTGLGNLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFGLSST 120
QY 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGMGFKFYQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGMGFKFYQYCPG 180
QY 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVTLATVLCNLGAMRNLYAMHRLQRPRSC 240
DB 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVTLATVLCNLGAMRNLYAMHRLQRPRSC 240
QY 241 RDCAEPRADGREGASPOPLEEDHLLALLMTVLTWCSLPVI 282
DB 241 RDCAEPRADGREGASPOPLEEDHLLALLMTVLTWCSLPVI 282
RESULT 2
AAW79009
ID AAW79009 standard; protein; 359 AA.
XX
AC AAW79009;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1671.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
FN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAK52142.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
```

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PS
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 359 AA;
Query Match 95.2%; Score 1467; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPYRCQNTTSVEKGNQAVMGVLFSTGLGNLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPYRCQNTTSVEKGNQAVMGVLFSTGLGNLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFGLSST 120
QY 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGMGFKFYQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGMGFKFYQYCPG 180
QY 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVTLATVLCNLGAMRNLYAMHRLQRPRSC 240
DB 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVTLATVLCNLGAMRNLYAMHRLQRPRSC 240
QY 241 RDCAEPRADGREGASPOPLEEDHLLALLMTVLTWCSLPVI 282
DB 241 RDCAEPRADGREGASPOPLEEDHLLALLMTVLTWCSLPVI 282
RESULT 3
ABP81901
ID ABP81901 standard; protein; 359 AA.
XX
AC ABP81901;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human prostaglandin D2 receptor protein SEQ ID NO:287.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
```


Db 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLLGNLLALGLLARSGLGWCRRPLRLPLSV 60
 QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120
 Db 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120
 QY 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGKFKFYQYCPG 180
 Db 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGKFKFYQYCPG 180
 QY 181 TWCFTQMVHEEGSLVGLGYSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRHPRST 240
 Db 181 TWCFTQMVHEEGSLVGLGYSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRHPRST 240
 QY 241 RDCAPRADGREASQPLEELDHLHLLALMTVLTWCSLPVI 282
 Db 241 RDCAPRADGREASQPLEELDHLHLLALMTVLTWCSLPVI 282

RESULT 5

ADO29614
 ID ADO29614 standard; protein; 359 AA.

XX ADO29614;

XX 29-JUL-2004 (first entry)

DE Human GPCR PTGDR, SEQ ID NO:716.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW skin disorder; uterus disorder; prostate disorder; testis disorder;
 KW ovary disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antiemetic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antieborrheic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX Madisen L, McGilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX N-PSDB; ADO30026.

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 716; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to

CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 359 AA;

Query Match 95.2%; Score 1467; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 1.6e-147; Indels 0; Gaps 0;

Matches 282; Conservative 0; Mismatches 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLLGNLLALGLLARSGLGWCRRPLRLPLSV 60

Db 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLLGNLLALGLLARSGLGWCRRPLRLPLSV 60

QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120

Db 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120

QY 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGKFKFYQYCPG 180

Db 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGKFKFYQYCPG 180

QY 181 TWCFTQMVHEEGSLVGLGYSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRHPRST 240

Db 181 TWCFTQMVHEEGSLVGLGYSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRHPRST 240

QY 241 RDCAPRADGREASQPLEELDHLHLLALMTVLTWCSLPVI 282

Db 241 RDCAPRADGREASQPLEELDHLHLLALMTVLTWCSLPVI 282

RESULT 6

AA94346

ID AA94346 standard; protein; 369 AA.

XX AA94346;

XX 22-AUG-2000 (first entry)

XX Human cell surface receptor protein #13.

XX Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
 KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
 KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
 KW Alzheimer's diseases; multiple sclerosis; epilepsy.

OS Homo sapiens.
 XX Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..47 /label= Signal_peptide
 FT Region
 FT 6..20 /note= "Prostaglandin D receptor"
 FT Region
 FT 10..57 /note= "2 Poly-Immunoglobulin receptor"
 FT Region
 FT 10 /note= "potential glycosylation site"
 FT Region
 FT 11..58 /note= "2 Poly-Immunoglobulin receptor"
 FT Region
 FT 12 /note= "potential phosphorylation site"
 FT Region
 FT 33..280 /note= "7 Transmembrane receptor"
 FT Region
 FT 41..58 /note= "Prostaglandin D receptor"
 FT Protein
 FT 48..369 /label= HCSR-13
 FT Region
 FT 50 /note= "potential phosphorylation site"
 FT Region
 FT 52..99 /note= "2 Poly-Immunoglobulin receptor"
 FT Region
 FT 69 /note= "potential phosphorylation site"
 FT Region
 FT 90 /note= "potential glycosylation site"
 FT Region
 FT 92 /note= "potential phosphorylation site"
 FT Region
 FT 93..104 /note= "Prostaglandin D receptor"
 FT Domain
 FT 144..161 /label= Transmembrane_domain
 FT Region
 FT 145 /note= "potential phosphorylation site"
 FT Region
 FT 185..200 /note= "Prostaglandin D receptor"
 FT Region
 FT 195..225 /note= "2 Poly-Immunoglobulin receptor"
 FT Domain
 FT 196..219 /label= Transmembrane_domain
 FT Region
 FT 236..259 /note= "Prostaglandin D receptor"
 FT Domain
 FT 264..283 /label= Transmembrane_domain
 FT Region
 FT 280..291 /note= "Prostaglandin D receptor"
 FT Region
 FT 297 /note= "potential glycosylation site"
 FT Region
 FT 299 /note= "potential phosphorylation site"
 FT Region
 FT 312 /note= "potential phosphorylation site"
 FT Region
 FT 330 /note= "potential phosphorylation site"
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 FT 346 /note= "potential phosphorylation site"
 XX WO200028032-A2.
 XX
 XX 18-MAY-2000.
 XX
 XX 12-NOV-1999; 99NO-US026742.
 XX
 XX 12-NOV-1998; 98US-00191280.
 PR 07-DEC-1998; 98US-00206647.
 PR 08-MAR-1999; 99US-0123404P.
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;

PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
 XX WPI; 2000-376546/32.
 DR N-PSDB; AAA27056.
 XX
 XX New human cell surface receptor protein and polynucleotide useful for
 PT diagnosis, prevention and treatment of cancer, immune disorders,
 FT infection and neuronal disorders.
 XX
 PS Claim 1; Page 87-88; 97pp; English.
 XX
 CC The present sequence is a novel human cell surface receptor protein
 CC (HCSR-13) designated HCSR-13. The nucleotide sequence was identified in
 CC Incyte Clone 3576503 from the cDNA library BRONNOT01, which was made from
 CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
 CC to assemble the consensus sequence. BLAST analysis showed that the
 CC sequence is homologous to DR prostanoil receptor g940379. HCSR-13 and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR-13. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HCSR-13 may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR-13 antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR-13
 CC and for diagnosis of HCSR-13-related disorders. HCSR-13 and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds
 XX
 SQ Sequence 369 AA;
 Query Match 95.2%; Score 1467; DB 3; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.7e-147;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLPLPSV 60
 DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLPLPSV 60
 QY 61 FYMLVGLTVTDLLGKCLLSPVVLAAYQNRSLRVLPALDNLCOAFEFNSFGLSST 120
 DB 61 FYMLVGLTVTDLLGKCLLSPVVLAAYQNRSLRVLPALDNLCOAFEFNSFGLSST 120
 QY 121 LQLLAMALECMLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
 DB 121 LQLLAMALECMLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
 QY 181 TWCFTQMVHEGSLSVLGYSVLYSSLMALLVLTATVLCNLGAMRNLYAMHRRILQRHPRST 240
 DB 181 TWCFTQMVHEGSLSVLGYSVLYSSLMALLVLTATVLCNLGAMRNLYAMHRRILQRHPRST 240
 QY 241 RDCAEPRADGREGASPOPLEELDHLHLLALMTVLTMCSLPVI 282
 DB 241 RDCAEPRADGREGASPOPLEELDHLHLLALMTVLTMCSLPVI 282
 RESULT 7
 ABB12000
 ID ABB12000 standard; peptide; 399 AA.
 XX
 AC ABB12000;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human prostaglandin DP receptor homologue, SEQ ID NO:2370.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

Chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US003800.

03-FEB-2000; 2000US-00496914.

27-APR-2000; 2000US-00560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49.

N-PSDB; ABA09244.

Human proteins and DNA encoding sequences useful for preventing, treating
or ameliorating a medical condition in a mammalian subject e.g. arthritis
and cancer.

Claim 20; Page 294; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
invention also relates to vectors and recombinant host cells comprising a
nucleotide of the invention, methods of producing the novel polypeptides,
antibodies against the polypeptides, methods of detecting the nucleotides
or polypeptides in a sample, and methods of identifying compounds which
bind to polypeptides of the invention. Although novel, many of the
polypeptides of the invention have homology to known proteins, thereby
giving an insight into their probable biological activities, and hence
potential therapeutic applications. The polypeptides of the invention may
have various activities, including cytokine, cell proliferation or cell
differentiation activities; stem cell growth factor activity;
haematopoiesis regulatory activity; tissue growth activity;
immunomodulatory activity; activin- or inhibin-related activities;
chemotactic or chemokinetic activities; haemostatic, thrombotic or
thrombolytic activities; receptor or ligand activities; or may be
involved in oncogenesis, cancer cell proliferation or metastasis.
Depending on their biological activities, polypeptides and nucleotides of
the invention are useful for preventing, treating or ameliorating medical
conditions, e.g., by protein or gene therapy. Such conditions include
cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
proliferative retinopathy, atherosclerosis, coronary heart disease,
arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
vascular growth. Polypeptides involved with tissue regeneration and
repair (or nucleic acids encoding them) may be used to promote wound
healing (e.g., of burns, incisions and ulcers), while those with
immunomodulatory activities may be used in the treatment of viral,
bacterial and fungal infections in addition to immune disorders.
Polypeptides with growth factor activity may be used in cell cultures to
promote cell growth. For example, such polypeptides may be used to
manipulate stem cells in culture to give rise to neuroepithelial cells
that can be used to augment or replace cells damaged by illness,
autoimmune disease or accidental damage. The polypeptides and nucleotides
may also be used in the diagnosis of the above conditions, and in drug
screening techniques. The present sequence represents a novel human
polypeptide of the invention

Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSPYRCQNTTSVEKGNASVMGVLFSTGLLGNLLALGLLARSGLGWCSPRLPLPSV 60
Db 41 MKSPYRCQNTTSVEKGNASVMGVLFSTGLLGNLLALGLLARSGLGWCSPRLPLPSV 100
Qy 61 FYMLVCGITVTDLGKCLLSPVVLAAYQNRSLRVLAPALDNLSCQAFPMFFSFFGLSST 120
Db 101 FYMLVCGITVTDLGKCLLSPVVLAAYQNRSLRVLAPALDNLSCQAFPMFFSFFGLSST 160
Qy 121 LQLLMALECMWLSLGHPPFFYRRHITRLGALVAPVVSFAFLCPMFGKFFVQYCPG 180
Db 161 LQLLMALECMWLSLGHPPFFYRRHITRLGALVAPVVSFAFLCPMFGKFFVQYCPG 220
Qy 181 TWCFTQMVHEEGSLSVLYGYSVLYSSIMALLVATVLCNLGMRNLYAMHRLQRPRSC 240
Db 221 TWCFTQMVHEEGSLSVLYGYSVLYSSIMALLVATVLCNLGMRNLYAMHRLQRPRSC 280
Qy 241 RDCAEPRADGREASPOPLEELDHLLALLMTVLTMTCSLPVI 282
Db 281 RDCAEPRADGREASPOPLEELDHLLALLMTVLTMTCSLPVI 322

RESULT 8
AAM79993
ID AAM79993 standard; protein; 399 AA.
AC AAM79993;
XX
XX 06-NOV-2001 (first entry)
XX Human protein SEQ ID NO 3639.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX Homo sapiens.
XX WO200157190-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US004098.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
XX N-PSDB; AAK53126.
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX Claim 20; Page 403-404; 6221pp; English.
XX The invention relates to polynucleotides (AAK531456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAAM80302) that exhibit activity relating to

CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLWCSSRRRLPLPSV 100
QY 61 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
DB 101 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAFMSFFGLSST 160
QY 121 LQLLAMALECWLISLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLAMALECWLISLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMRNLYAMHRRRLQHRPSCT 240
DB 221 TWCFIQMVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMRNLYAMHRRRLQHRPSCT 280
QY 241 RDCAEPRADGREALSPQLELDHLLALMTVLTMCSLPVI 282
DB 281 RDCAEPRADGREALSPQLELDHLLALMTVLTMCSLPVI 322

RESULT 9
ADE09040
ID ADE09040 standard; protein; 399 AA.

XX ADE09040;

XX 29-JAN-2004 (first entry)

XX Novel protein-related contig polypeptide sequence #106.

DE novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; contig.

XX Unidentified.

XX WO2003054152-A2.

XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

XX 11-DEC-2001; 2001US-0339453P.

XX 14-MAR-2002; 2002US-0365091P.

XX 14-MAR-2002; 2002US-0365384P.

XX 12-APR-2002; 2002US-0372381P.

XX 12-APR-2002; 2002US-0372615P.

XX 24-APR-2002; 2002US-0376045P.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX WPI; 2003-569235/53.

XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.

XX Disclosure; SEQ ID NO 2584; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence was used in the
CC exemplification of the invention.

XX Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 7; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLWCSSRRRLPLPSV 100
QY 61 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
DB 101 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAFMSFFGLSST 160
QY 121 LQLLAMALECWLISLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLAMALECWLISLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMRNLYAMHRRRLQHRPSCT 240
DB 221 TWCFIQMVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMRNLYAMHRRRLQHRPSCT 280
QY 241 RDCAEPRADGREALSPQLELDHLLALMTVLTMCSLPVI 282
DB 281 RDCAEPRADGREALSPQLELDHLLALMTVLTMCSLPVI 322

RESULT 10

ADE07993
ID ADE07993 standard; protein; 424 AA.

XX ADE07993;

XX 29-JAN-2004 (first entry)

XX Novel protein (useful for identifying genetic disorders) #148.

DE novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.

XX Unidentified.

XX WO2003054152-A2.

XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

XX 11-DEC-2001; 2001US-0339453P.

XX 14-MAR-2002; 2002US-0365091P.

XX 14-MAR-2002; 2002US-0365384P.

XX 12-APR-2002; 2002US-0372381P.

XX 12-APR-2002; 2002US-0372615P.

CC This sequence represents the murine prostaglandin D receptor. The
CC encoding sequence was obtained through reverse transcription PCR (using
CC the primers represented by AAT05173-T05176). The full length DNA sequence
CC can be used in a vector to transform cells to produce this sequence. This
CC sequence can be used as an agent for the prevention and treatment of
CC diseases caused by excessive production of PGD-2, such as an immune
CC activator and an inhibitor of bleeding

XX Sequence 357 AA;
Query Match 71.3%; Score 1099; DB 2; Length 357;
Best Local Similarity 75.8%; Pred. No. 3.1e-108;
Matches 210; Conservative 26; Mismatches 41; Indels 0; Gaps 0;
QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGCRRPLRLPSPVYMLV 65
DB 5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGCRRPLRLPSPVYMLV 64
QY 66 CGLTVDLLGKCLSPVLAAYQAQRSLRVLPALDNLSCQAFPMFSGFLSSTLQLLA 125
DB 65 CGLTVDLLGKCLSPVLAAYQAQRSLRVLPALDNLSCQAFPMFSGFLSSTLQLLA 124
QY 126 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFLAFPCALPFGKVFQVCPGTWCPI 185
DB 125 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFLAFPCALPFGKVFQVCPGTWCPI 184
QY 186 QMVHEEGSLVGLSVLYSSLMALLVATVLCNGLGMRNLYAMHRLQHPHRSCTRDCAE 245
DB 185 QMVHEEGSLVGLSVLYSSLMALLVATVLCNGLGMRNLYAMHRLQHPHRSCTRDCAE 244
QY 246 PRADG---REASPOPLELHLLALMTVLTMCSLPVI 282
DB 245 SGGDYRHGSLHLELDFHLLALMTVLTMCSLPVI 281

RESULT 14
ADO29619
ID ADO29619 standard; protein; 362 AA.
AC ADO29619;
XX
XX 29-JUL-2004 (first entry)
XX
XX Mouse GPCR PTGER2, SEQ ID NO:721.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antiangiinal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; receptor.

XX Mus musculus.
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.

XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR N-PSDB; ADO30318.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 721; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 362 AA;
Query Match 38.6%; Score 595.5; DB 8; Length 362;
Best Local Similarity 45.4%; Pred. No. 1.7e-54;
Matches 128; Conservative 50; Mismatches 87; Indels 17; Gaps 7;
QY 8 CONTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCRRPLRLPSPVYMLV 65
DB 14 CKSRQWLLSGSPATSSVYMFAGVLGNLIALALLARRWRGDTGCCSAGS-RTSISLPHVLV 72
QY 66 CGLTVDLLGKCLSPVLAAYQAQRSLRVLPALDNLSCQAFPMFSGFLSSTLQLLA 125
DB 73 TELVTDLGCLSPVLAAYQAQRSLRVLPALDNLSCQAFPMFSGFLSSTLQLLA 130
QY 126 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFLAFPCALPFGKVFQVCPGTWCPI 185
DB 131 MALERYLSIGVPYFRRHLSRRGGLAVLVFYVAGSLLFCSLPPLLNGEYVQVCPGTWCPI 190
QY 186 QMVHEEGSLVGLSVLYSSLMALLVATVLCNGLGMRNLYAMHRLQHPHRSCTRDCAE 245
DB 191 R--HGR-----TAYLQLYATVMTLLLVAVLACNISVILNIRMHRSRR--SRCCGLSGSS 241
QY 246 PRADG---REASPOPLELHLLALMTVLTMCSLPVI 284
DB 242 LRPGSRRRGERTSMAETDHLILALMTVLTMCSLPVI 283

RESULT 15

ABP81903
ID ABP81903 standard; protein; 358 AA.
XX AC
XX ABP81903;
XX DT
XX 04-MAR-2003 (first entry)
XX DE Human prostaglandin E receptor EP2 protein SEQ ID NO:291.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

XX OS
XX WO200261087-A2.

XX PD
XX 08-AUG-2002.

XX PF
XX 19-DEC-2001; 2001WO-US050107.

XX PR
XX 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burmer GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX DR N-PSDB; AB242750.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 358 AA;

XX SQ

Query Match 38.0%; Score 586; DB 6; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.8e-53;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLLALGILARSGLG--WCSSRPRLPLPSVFMVLV 65
DB 13 CETROQLPPGESPAISSVMFSGVLGNLTALARRWRGDCSAGRSSL-SLPHVLV 71
QY 66 CGLTVTDLIGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFESLATMLMFA 129
QY 126 MALECWLSLGHFFVRRHITLRLGALVAPVVSFAFLAFCALPFMGKGFVQVCPGTWCFT 185
DB 130 MALERYLSIGHFYFYQRRVSASGGLAVLPVIYAVSLLFCSLPLLDYGVVQVCPGTWCFT 189
QY 186 QMVHEEGSLSVLGYSVLYSSLMALLVLAIVLNLGAMRNLYAMHRELQRPSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLTLILLIVSLACNFVILNLRMHRRSR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLLLALMTVLFTWCSLPVI AF 284
DB 241 GRGFCARRRGERSVMAEETHLILLAINITITFAVCSLPFTIF 283

Search completed: April 22, 2005, 21:27:23

Job time : 57.229 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:00:43 ; Search time 17.6244 Seconds
(without alignments)
1253.721 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVPGVPAKTPGSR 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
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4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1467	95.2	359	2 US-08-812-203-3	Sequence 3, Appli
2	1467	95.2	359	3 US-09-300-864-3	Sequence 3, Appli
3	1467	95.2	359	3 US-09-598-418-3	Sequence 3, Appli
4	585	38.0	358	1 US-08-239-431A-4	Sequence 4, Appli
5	585	38.0	358	1 US-09-267-423-4	Sequence 4, Appli
6	580	37.6	358	4 US-09-826-509-559	Sequence 559, App
7	564	36.6	358	2 US-08-463-0818-6	Sequence 6, Appli
8	564	36.6	358	2 US-08-461-378A-6	Sequence 6, Appli
9	564	36.6	358	2 US-08-462-390B-6	Sequence 6, Appli
10	564	36.6	358	2 US-08-463-074B-6	Sequence 6, Appli
11	564	36.6	358	3 US-08-465-585C-6	Sequence 6, Appli
12	564	36.6	358	3 US-08-652-446-6	Sequence 6, Appli
13	518.5	33.6	386	1 US-08-134-012-3	Sequence 3, Appli
14	518.5	33.6	386	1 US-08-520-513-3	Sequence 3, Appli
15	518.5	33.6	386	3 US-09-039-798-3	Sequence 3, Appli
16	389	25.2	513	1 US-08-390-162-6	Sequence 6, Appli
17	389	25.2	513	1 US-08-685-945B-6	Sequence 6, Appli
18	364.5	23.7	488	1 US-08-115-365-2	Sequence 2, Appli
19	364.5	23.7	488	1 US-08-586-897-2	Sequence 2, Appli
20	361.5	23.5	488	4 US-09-826-509-561	Sequence 561, App
21	261.5	17.0	361	1 US-08-390-162-4	Sequence 4, Appli
22	261.5	17.0	361	1 US-08-685-945B-4	Sequence 4, Appli
23	261.5	17.0	365	1 US-08-390-162-2	Sequence 2, Appli
24	261.5	17.0	365	1 US-08-685-945B-2	Sequence 2, Appli
25	256	16.6	385	1 US-08-416-758A-3	Sequence 3, Appli
26	256	16.6	385	4 US-08-880-863-3	Sequence 3, Appli
27	250.5	16.3	343	4 US-09-054-272-6	Sequence 6, Appli

28 244.5 15.9 365 3 US-08-155-005A-8 Sequence 8, Appli
29 244.5 15.9 365 3 US-09-363-783-8 Sequence 8, Appli
30 244.5 15.9 365 4 US-09-661-758A-8 Sequence 8, Appli
31 244.5 15.9 388 3 US-08-155-005A-6 Sequence 6, Appli
32 244.5 15.9 388 3 US-09-363-783-6 Sequence 6, Appli
33 244.5 15.9 388 4 US-09-661-758A-6 Sequence 6, Appli
34 244.5 15.9 390 3 US-08-155-005A-4 Sequence 4, Appli
35 244.5 15.9 390 3 US-08-155-005A-17 Sequence 17, Appli
36 244.5 15.9 390 3 US-09-363-783-4 Sequence 4, Appli
37 244.5 15.9 390 3 US-09-363-783-17 Sequence 17, Appli
38 244.5 15.9 390 4 US-09-661-758A-4 Sequence 4, Appli
39 244.5 15.9 390 4 US-09-661-758A-17 Sequence 17, Appli
40 225.5 14.6 378 1 US-08-416-758A-4 Sequence 4, Appli
41 225.5 14.6 378 4 US-08-880-863-4 Sequence 4, Appli
42 219.5 14.2 402 2 US-08-068-729-4 Sequence 4, Appli
43 219.5 14.2 402 3 US-09-255-671-4 Sequence 4, Appli
44 219.5 14.2 402 4 US-09-395-366-4 Sequence 4, Appli
45 219.5 14.2 402 4 US-09-826-509-557 Sequence 557, App

ALIGNMENTS

RESULT 1
US-08-812-203-3
; Sequence 3, Application US/08812203
; Patent No. 5958723
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/812,203
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-203-3

Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAMSPFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAMSPFGLSST 120
QY 121 LQLLAMALECWLGLHPFFRYRRHITLRLGALVAPVVSFAFLAFALPFGFGKFFVOYCPG 180
DB 121 LQLLAMALECWLGLHPFFRYRRHITLRLGALVAPVVSFAFLAFALPFGFGKFFVOYCPG 180
QY 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
DB 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
QY 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTMCSLPVI 282
DB 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTMCSLPVI 282

RESULT 2

US-09-300-864-3
; Sequence 3, Application US/09300864
; Patent No. 6214972
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,864
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-300-864-3

Query Match 95.2%; Score 1467; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAMSPFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAMSPFGLSST 120
QY 121 LQLLAMALECWLGLHPFFRYRRHITLRLGALVAPVVSFAFLAFALPFGFGKFFVOYCPG 180
DB 121 LQLLAMALECWLGLHPFFRYRRHITLRLGALVAPVVSFAFLAFALPFGFGKFFVOYCPG 180
QY 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
DB 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
QY 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTMCSLPVI 282
DB 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTMCSLPVI 282

RESULT 3
US-09-598-418-3
; Sequence 3, Application US/09598418
; Patent No. 6395499
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,418
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-598-418-3

Query Match 95.2%; Score 1467; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60

QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LOLLAMALECWLGLGHPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPG 180
DB 121 LOLLAMALECWLGLGHPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPG 180
QY 181 TWCFFIQMHVEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRRLQRHPRSC 240
DB 181 TWCFFIQMHVEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRRLQRHPRSC 240
QY 241 RDCASPRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 282
DB 241 RDCASPRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 282

RESULT 4

US-08-239-431A-4
; Sequence 4, Application US/08239431A
; Patent No. 5716835
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; TITLE OF INVENTION: NOVEL HUMAN EP PROTAGLANDIN RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,431A
; FILING DATE: 05-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: ALRGN.053A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-239-431A-4

Query Match 38.0%; Score 585; DB 1; Length 358;
Best Local Similarity 45.2%; Pred. No. 2,2e-47;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CONTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCRRRLRPLPSVFMVLV 65

DB 13 CETROWLPPGESPAISSVMFSGVLGNLTALALLARRWRGDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 72 TELVFTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPGTCFI 185
DB 130 MALERYLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPGTCFI 189
QY 186 QMVHEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRRLQRHPRSC 245
DB 190 R--HGR-----TAYLQLYATLTLIVSVLACNFSVILNLRHRRSR--SRCGSPSLGS 240
QY 246 ----PRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 284
DB 241 GRGGFGARRRGERSVMAEETHLILLAITITFAVCSLPFTIF 283

RESULT 5

US-09-267-423-4
; Sequence 4, Application US/09267423
; Patent No. 6395878
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; TITLE OF INVENTION: No. 6395878el Human Prostaglandin EP Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/09/267,423
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 09/019,393
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: 08/239,431
; EARLIER FILING DATE: 1994-05-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-267-423-4

Query Match 38.0%; Score 585; DB 3; Length 358;
Best Local Similarity 45.2%; Pred. No. 2,2e-47;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CONTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCRRRLRPLPSVFMVLV 65
DB 13 CETROWLPPGESPAISSVMFSGVLGNLTALALLARRWRGDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 72 TELVFTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPGTCFI 185
DB 130 MALERYLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFPCALPFMGFGKFGVQYCPGTCFI 189
QY 186 QMVHEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRRLQRHPRSC 245
DB 190 R--HGR-----TAYLQLYATLTLIVSVLACNFSVILNLRHRRSR--SRCGSPSLGS 240
QY 246 ----PRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 284
DB 241 GRGGFGARRRGERSVMAEETHLILLAITITFAVCSLPFTIF 283

RESULT 6

US-09-826-509-559
; Sequence 559, Application US/09826509
; Patent No. 6806054

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; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brunnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-559

Query Match      37.6%; Score 580; DB 4; Length 358;
Best Local Similarity 44.9%; Pred. No. 6.5e-47;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY      8  CONTTSVEKGSAAVGGVLFSTGLGALLLALLGALLARSGLG--WCSRRRLRLPLPSVYFVMLV 65
Db      13  CETRWLPFGSPALSSVWFSGVGNLIALALLARRWGDVGCAGRRSSL-SLFHVLV 71
QY      66  CGLTVTDLGKCLLSPVVLAAAYQNRSLRVLPALDNLSCQAFPMFSGFGLSSTLQLLA 125
Db      72  TELVFTDLGLTCLISPVVLASVARNQTLVALAP--ESRACTVFAFAMTFSSLATMMLFA 129
QY      126  MALECWLSLGHPPFRRHITLRLGALVAPVVSAPSLAFALCPFMFGFKVQYCPGTWCFI 185
Db      130  MALERYLSLGHPIFYQRRVSAGGLAVLPVIYAVSLFCSLPDLLDYGQYVQYCPGTWCFI 189
QY      186  QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMNLYAMHRRRLQHRPRSCTRDCAE 245
Db      190  R--HGR-----TAYLQLVATLILLIVSVLACNFSVILNLRMHRRSRR--SRCGPSLGS 240
QY      246  ----PRADGRASPOPLELDHLLALLMTVLTWCSLPVIAT 284
Db      241  GRGGFGARRRGERSVMAEETDKILLAIWITTFVAVCSLPFTIF 283

RESULT 7
US-08-463-081B-6
; Sequence 6, Application US/08463081B
; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: USSN 08/330,108; 08/104,736
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; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-081B-6

Query Match      36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;

QY      8  CONTTSVEKGSAAVGGVLFSTGLGALLLALLGALLARSGLG--WCSRRRLRLPLPSVYFVMLV 65
Db      13  CETRWLPFGSPALSSVWFSGVGNLIALALLARRWGDVGCAGRRSSL-SLFHVLV 71
QY      66  CGLTVTDLGKCLLSPVVLAAAYQNRSLRVLPALDNLSCQAFPMFSGFGLSSTLQLLA 125
Db      72  TELVFTDLGLTCLISPVVLASVARNQTLVALAP--ESRACTVFAFAMTFSSLATMMLFT 129
QY      126  MALECWLSLGHPPFRRHITLRLGALVAPVVSAPSLAFALCPFMFGFKVQYCPGTWCFI 185
Db      130  MALERYLSLGHPIFYQRRVSAGGLAVLPVIYAVSLFCSLPDLLDYGQYVQYCPGTWCFI 189
QY      186  QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMNLYAMHRRRLQHRPRSCTRDCAE 245
Db      190  R--HGR-----TAYLQLVATLILLIVSVLACNFSVILNLRMHRRSRR--SRCGPSLGS 240
QY      246  ----PRADGRASPOPLELDHLLALLMTVLTWCSLPVIAT 284
Db      241  GRGGFGARRRGERSVMAEETDKILLAIWITTFVAVCSLPFTIF 283

RESULT 8
US-08-461-379A-6
; Sequence 6, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: USSN 08/330,108; 08/104,736
```

APPLICATION NUMBER: 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-379A-6

Query Match 36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 CQNTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCSRRLRLPLPSVFMVLV 65
DB 13 CTRQWFPFGESPAISSVMFSGVLNLIETALLARRWQDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVDLGLKLLSPVLAAYAQNRSLRVLPALDNLCOAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLGLTCLISPVVLASYARNQTLVALAP--ESRASYTFAPAMTFFSLATMLMLFT 129
QY 126 MALECHWSLGHFFYRRHTLRLGALVAPVVSFAFLAFALPMGKFGKVCPTWCPI 185
DB 130 MALERYLSIGHFYFQRRVSRSGGLAVLPVIYAVSLFLCSLPLLDYGQVQVCPGTWCPI 189
QY 186 QMVHEEGSLVGLSYSLMALVLTATVLCNLGAMRNLYAMHRLQRHPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLALLLVSVLACNFSVILNIRHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLFTMCSLPIAF 284
DB 241 GRGGPGARRGRVSMAEETHLLAILMTITFAVCSLPFTIF 283

RESULT 9
US-08-462-390B-6
Sequence 6, Application US/08462390B
Patent No. 5832894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ADDRESS: (B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-390B-6
Query Match 36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 CQNTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCSRRLRLPLPSVFMVLV 65
DB 13 CTRQWFPFGESPAISSVMFSGVLNLIETALLARRWQDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVDLGLKLLSPVLAAYAQNRSLRVLPALDNLCOAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLGLTCLISPVVLASYARNQTLVALAP--ESRASYTFAPAMTFFSLATMLMLFT 129
QY 126 MALECHWSLGHFFYRRHTLRLGALVAPVVSFAFLAFALPMGKFGKVCPTWCPI 185
DB 130 MALERYLSIGHFYFQRRVSRSGGLAVLPVIYAVSLFLCSLPLLDYGQVQVCPGTWCPI 189
QY 186 QMVHEEGSLVGLSYSLMALVLTATVLCNLGAMRNLYAMHRLQRHPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLALLLVSVLACNFSVILNIRHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLFTMCSLPIAF 284
DB 241 GRGGPGARRGRVSMAEETHLLAILMTITFAVCSLPFTIF 283

RESULT 10
US-08-463-074B-6
Sequence 6, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
444 South Flower St. - Suite 1900

APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-446-6

Query Match 36.6%; Score 564; DB 3; Length 358;

Best Local Similarity 44.2%; Pred. No. 2.1e-45;

Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;

QY 8 CONTTSVEKGNVAVMGVLFSTGLGNLALGLLARSGLG--WCSRRPLRLPSVYMLV 65
DB 13 CETROFFPGESPAISVNFSAVLGNLIELALLARRWQGVGCSAGRESSL-SLPHVLV 71
QY 66 CGLVTDLGKCLSPVLLAAVQNSRLVAPALDNLSCQAFAPMSPFGLSSTLQLLA 125
DB 72 TELVFTDLGTCISPVLLASTARNLVALAP--ESRASTVPAPANTFSLATMLMLFT 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFGKFGVQYCPGTWCFI 185
DB 130 MALERYLSIGHPPFYQRRYSRGLAVLPVIYAVSLFLCSLPLLDYQYVQYCPGTWCFI 189
QY 186 QMVHEGSLVSLVGYSLVSLMALLVATVLCNLGAMRNLYAMHRLQRHPRSCRTDCAE 245
DB 190 R--HGR-----TAYLQVATLILLVSVLACNFSVILNIRHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASQPLELDHLLALMTVLTMCSLPVIAP 284
DB 241 GRGPGARRRGERSVMAEETHLLILALMTITFAVCSLPFTIF 283

RESULT 13

US-08-134-012-3

Sequence 3, Application US/08134012

Patent No. 5516652

GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark

APPLICANT: Boie, Yves

APPLICANT: Grygorczyk, Richard

APPLICANT: Metters, Kathleen

APPLICANT: Rushmore, Thomas H.

APPLICANT: Slipetz, Deborah M.

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: John Wallen

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-OCT-1993
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-134-012-3

Query Match 33.6%; Score 518.5; DB 1; Length 386;

Best Local Similarity 43.3%; Pred. No. 4.7e-41;

Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGNVAVMGVLFSTGLGNLALGLLARSGLGWSRRRLRLPSVYMLVCG 67
DB 5 CRNLTVRGSGVATSTLMFVAGVGVNGLAIGLS-----ARRPAR--PSAFAVLVTG 55
QY 68 LVTDLGKCLSPVLLAAVQNSRLVLA---PALDNLSCQAFAPMSPFGLSSTLQLL 124
DB 56 LAATDLGTSFSLPFAVFAVARNSSLGLARGPA---LCDAFAPAMTFFGLASMLILF 111
QY 125 ANALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFGKFGVQYCPGTWCF 184
DB 112 ANAVERCIALSPYLYAQDGPGRCARLALPAIYAFCLVLCALPLGLGQHQYCPGWSWF 171
QY 185 IQM--VHEGSLVSLVGYSLVSLMALLVATVLCNLGAMRNLYAMHRLQRHPRSCRTD 242
DB 172 LRMRWAQPGA---AFSLAYAGVALLVAALFLCNGSVTLSCRMVYRQQRHQGS---- 223
QY 243 CAERADGREASQPL---EELDHLILLALMTVLTMCSLPV 281
DB 224 -----LGPRPRTEGDEVDHLLILALMTVVMVAVCSLPL 255

RESULT 14

US-08-520-519-3

Sequence 3, Application US/08520519

Patent No. 5728808

GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark

APPLICANT: Boie, Yves

APPLICANT: Grygorczyk, Richard

APPLICANT: Metters, Kathleen

APPLICANT: Rushmore, Thomas H.

APPLICANT: Slipetz, Deborah M.

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jack L. Tribble

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:29:33 ; Search time 153.649 Seconds
(without alignments)
641.112 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVPGVPKTPGSR 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1467	95.2	359	14	US-10-225-567A-287
2	1467	95.2	359	15	US-10-276-774-2370
3	586	38.0	358	14	US-10-225-567A-291
4	586	38.0	358	15	US-10-352-684A-36
5	586	38.0	358	15	US-10-366-288-36
6	586	38.0	358	16	US-10-755-889-92
7	585	38.0	358	17	US-10-108-714-4
8	585	38.0	358	17	US-10-684-206-38
9	580	37.6	358	17	US-09-826-509-559
10	580	37.6	358	17	US-10-925-095-559
11	518.5	33.6	289	15	US-10-108-260A-3907
12	518.5	33.6	386	14	US-10-225-567A-285
13	364.5	23.7	488	14	US-10-225-567A-296

14	364.5	23.7	488	14	US-10-320-351-3	Sequence 3, Appli
15	364.5	23.7	488	15	US-10-295-027-1326	Sequence 1326, Ap
16	364.5	23.7	488	16	US-10-755-889-170	Sequence 170, App
17	363.5	23.6	490	14	US-10-243-501-3	Sequence 3, Appli
18	361.5	23.5	488	10	US-09-826-509-561	Sequence 561, App
19	361.5	23.5	488	17	US-10-925-095-561	Sequence 561, App
20	361.5	23.5	490	14	US-10-243-351-2	Sequence 2, Appli
21	250.5	16.3	328	13	US-10-087-192-204	Sequence 204, App
22	250.5	16.3	343	14	US-10-225-567A-448	Sequence 448, App
23	250.5	16.3	343	16	US-10-755-889-596	Sequence 596, App
24	250.5	16.3	369	16	US-10-408-765A-176	Sequence 176, App
25	250.5	16.3	407	14	US-10-198-070-104	Sequence 104, App
26	244.5	15.9	365	14	US-10-060-902-32	Sequence 32, Appl
27	244.5	15.9	365	15	US-10-354-247-32	Sequence 32, Appl
28	244.5	15.9	374	14	US-10-060-902-30	Sequence 30, Appl
29	244.5	15.9	374	15	US-10-354-247-30	Sequence 30, Appl
30	244.5	15.9	388	14	US-10-060-902-16	Sequence 16, Appl
31	244.5	15.9	388	15	US-10-354-247-16	Sequence 16, Appl
32	244.5	15.9	390	14	US-10-060-902-22	Sequence 22, Appl
33	244.5	15.9	390	14	US-10-060-902-24	Sequence 24, Appl
34	244.5	15.9	390	15	US-10-354-247-22	Sequence 22, Appl
35	244.5	15.9	390	15	US-10-354-247-24	Sequence 24, Appl
36	244.5	15.9	393	14	US-10-060-902-28	Sequence 28, Appl
37	244.5	15.9	393	14	US-10-060-902-36	Sequence 36, Appl
38	244.5	15.9	393	15	US-10-354-247-28	Sequence 28, Appl
39	244.5	15.9	393	15	US-10-354-247-36	Sequence 36, Appl
40	244.5	15.9	402	14	US-10-225-567A-294	Sequence 294, App
41	244.5	15.9	402	14	US-10-060-902-34	Sequence 34, Appl
42	244.5	15.9	407	14	US-10-354-247-34	Sequence 34, Appl
43	244.5	15.9	407	14	US-10-060-902-18	Sequence 18, Appl
44	244.5	15.9	407	15	US-10-354-247-18	Sequence 18, Appl
45	244.5	15.9	425	14	US-10-060-902-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-287
; Sequence 287, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 287
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-287

Query Match	95.2%	Score 1467;	DB 14;	Length 359;
Best Local Similarity	100.0%;	Pred. No. 5.9e-134;		
Matches 282;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKSPYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSPRLPLPSV	60	
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Qy	61	FYMLVCGLTVDLLGKCLLSPVVLAAYQNSRLRVLPALDNLQCAFAMFFGLSST	120	
Db	61	FYMLVCGLTVDLLGKCLLSPVVLAAYQNSRLRVLPALDNLQCAFAMFFGLSST	120	
Qy	121	LQLLAMALECWLGLGHFFPYRRHITRLGALVAPVVSAPSLAFALPFMGFKVQYCPG	180	

Db 121 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFGVQYCPG 180
QY 181 TWCFTOMVHEEGSLVGLGVSYSSIMALLVLTATVLCNLGAMRNLYAMHRRLQHRPRST 240
Db 181 TWCFTOMVHEEGSLVGLGVSYSSIMALLVLTATVLCNLGAMRNLYAMHRRLQHRPRST 240
QY 241 RDCAPRADGRASPOPLELHLLALLMTVLTWCISLPVI 282
Db 241 RDCAPRADGRASPOPLELHLLALLMTVLTWCISLPVI 282

RESULT 2

US-10-276-774-2370
; Sequence 2370, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2370
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2370

Query Match 95.2%; Score 1467; DB 15; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.7e-134;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 41 MKSPFYRCNTTSVEKGSNAVGGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 100
QY 61 FYMLVGLTVTLGLKCLSPVVLAAQNRSLRVLPALDNLSCQAFPMFSGFLSST 120
Db 101 FYMLVGLTVTLGLKCLSPVVLAAQNRSLRVLPALDNLSCQAFPMFSGFLSST 160
QY 121 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFGVQYCPG 180
Db 161 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFGVQYCPG 220
QY 181 TWCFTOMVHEEGSLVGLGVSYSSIMALLVLTATVLCNLGAMRNLYAMHRRLQHRPRST 240
Db 221 TWCFTOMVHEEGSLVGLGVSYSSIMALLVLTATVLCNLGAMRNLYAMHRRLQHRPRST 280
QY 241 RDCAPRADGRASPOPLELHLLALLMTVLTWCISLPVI 282
Db 281 RDCAPRADGRASPOPLELHLLALLMTVLTWCISLPVI 322

RESULT 3

US-10-225-567A-291
; Sequence 291, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 291
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-291
Query Match 38.0%; Score 536; DB 14; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 QNTTSVEKGSNAVGGVLFSTGLGNLLALGLLARSGLG--WCRRPLRLPSVYFMYLV 65
Db 13 CETQWLPPGESPAISSVMFSGVGNLIALALLARRWGVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTLGLKCLSPVVLAAQNRSLRVLPALDNLSCQAFPMFSGFLSSTLQLLA 125
Db 72 TELVFTDLGLTCLSPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLLPA 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFGVQYCPGTWCFI 185
Db 130 MALERYLSIGHYPFYQRRVSASGGLAVLPVIYAVSLLFCSLPFLDYGOVQYVQYCPGTWCFI 189
QY 186 QMVEEGSLVGLGVSYSSIMALLVLTATVLCNLGAMRNLYAMHRRLQHRPRSTRDCAE 245
Db 190 R--HGR-----TAYLQLYATLULLLIVSVLACNFSVILNLRMHRRSR--SRCPSLGS 240
QY 246 ---PRADGRASPOPLELHLLALLMTVLTWCISLPVIAP 284
Db 241 GRGFGARRRRGERSMAEETHLLILLMTITFAVCSLPFTIF 283

RESULT 4

US-10-352-684A-36
; Sequence 36, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-0191RNMNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13

Query Match 38.0%; Score 586; DB 15; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;

RESULT 7
S-10-108-714-4

```
; Sequence 4, Application US/10108714
; Publication No. US20020128445A1
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: No. US20020128445A1el Human Prostaglandin EP Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/10/108,714
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-108-714-4

Query Match 38.0%; Score 585; DB 13; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.9e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 QNTTSVEKGSNAVMGVLFTSLGILNLLALGLLARSGLG--WCSRRPLRLPLSPVYFMYLV 65
DB 13 CETROWLPPEGSPALSSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAFMSFFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSASFALFCALPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGQVQVCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLEEHLHLLALMTVLFTMCSLPVIAP 284
DB 241 GRGGFGARRGERVSMAEETHLLAILAINTITFAVCSLPFTIF 283

RESULT 8
US-10-684-206-38
; Sequence 38, Application US/10684206
; Publication No. US20050032725A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Szymanska, Grazyna
; TITLE OF INVENTION: Molecules Associated With Regulatory T
; FILE REFERENCE: T1N-021CP
; CURRENT APPLICATION NUMBER: US/10/684,206
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/417102
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/417103
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/417243
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/419575
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/424777
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 358

QY 8 QNTTSVEKGSNAVMGVLFTSLGILNLLALGLLARSGLG--WCSRRPLRLPLSPVYFMYLV 65
DB 13 CETROWLPPEGSPALSSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAFMSFFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSASFALFCALPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGQVQVCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLEEHLHLLALMTVLFTMCSLPVIAP 284
DB 241 GRGGFGARRGERVSMAEETHLLAILAINTITFAVCSLPFTIF 283
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-684-206-38

Query Match 38.0%; Score 585; DB 17; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.9e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 QNTTSVEKGSNAVMGVLFTSLGILNLLALGLLARSGLG--WCSRRPLRLPLSPVYFMYLV 65
DB 13 CETROWLPPEGSPALSSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAFMSFFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSASFALFCALPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGQVQVCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLEEHLHLLALMTVLFTMCSLPVIAP 284
DB 241 GRGGFGARRGERVSMAEETHLLAILAINTITFAVCSLPFTIF 283

RESULT 9
US-09-826-509-559
; Sequence 559, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: ARN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-559

Query Match 37.6%; Score 580; DB 10; Length 358;
Best Local Similarity 44.9%; Pred. No. 8.9e-48;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY 8 QNTTSVEKGSNAVMGVLFTSLGILNLLALGLLARSGLG--WCSRRPLRLPLSPVYFMYLV 65
DB 13 CETROWLPPEGSPALSSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAFMSFFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSASFALFCALPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGQVQVCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
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QY 246 ----PRADGREGASPOPLELHLLALMTVLFTWCSLPVIAF 284
Db 241 GRGGPGARRRGERVSNABETHKILLAINMTITFAVCSLPFTTIF 283

RESULT 10

US-10-925-095-559
; Sequence 559, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-559

Query Match 37.6%; Score 580; DB 17; Length 358;
Best Local Similarity 44.9%; Pred. No. 8.9e-48;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLALGLLARSGLG--WCRRRPLRPLPSVFMVLV 65
Db 13 CETROWLPGESPAISVNFSGVLGNLALGLLARSGLG--WCRRRPLRPLPSVFMVLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLL 125
Db 72 TELVFTDGLTCLISPVVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLL 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFSLAFALFPMGFGKFOYCPGTWCFI 185
Db 130 MALERYLSIGHPPFYRRHITLRLGALVAPVVSFAFSLAFALFPMGFGKFOYCPGTWCFI 189
QY 186 QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTDCAE 245
Db 190 R--HGR-----TAYLQVATLALLLIVSVLACNFSVILNLRHRRSR--SRCGPGSLGS 240
QY 246 ----PRADGREGASPOPLELHLLALMTVLFTWCSLPVIAF 284
Db 241 GRGGPGARRRGERVSNABETHKILLAINMTITFAVCSLPFTTIF 283

RESULT 11

US-10-108-260A-3907
; Sequence 3907, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3907
; LENGTH: 289
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-108-260A-3907

Query Match 33.6%; Score 518.5; DB 15; Length 289;
Best Local Similarity 43.3%; Pred. No. 6.5e-42;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLALGLLARSGLGWCRRRPLRPLPSVFMVLVCG 67
Db 5 CRNLTYVRGSGVPATSTLTMFVAGVVGNGLALGILS-----ARRPAR--PSAFVLTG 55
QY 68 LTVTDLLGKCLLSPVLAAYQNRSLRVL-----PALDNLSCQAFAPFMSFFGLSSTLQLL 124
Db 56 LAATDGLTSLSPAVFVAYARNSSLGLARGGPA-----LCDAFAPAMTFFGLASMLILF 111
QY 125 AMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFSLAFALFPMGFGKFOYCPGTWCF 184
Db 112 AMAVERCLALSHPLYAQLDGPRCARLALPAIYAFVLCALPLLLGLGHOHQYCPGSMCF 171
QY 185 IQM--VHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTD 242
Db 172 LRMRWAQPGGA-----AFSLAYAGLVALLVAIFLCNCGSVTLSCRMRYQQRHOGS---- 223
QY 243 CAEPRADGREGASPOPL---EELDHLLALLALMTVLFTWCSLPV 281
Db 224 -----LGPRTGDEVDHLLALLALMTVVMVAVCSLP 255

RESULT 12

US-10-225-567A-285
; Sequence 285, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 285
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-285

Query Match 33.6%; Score 518.5; DB 14; Length 386;
Best Local Similarity 43.3%; Pred. No. 9.2e-42;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLALGLLARSGLGWCRRRPLRPLPSVFMVLVCG 67
Db 5 CRNLTYVRGSGVPATSTLTMFVAGVVGNGLALGILS-----ARRPAR--PSAFVLTG 55
QY 68 LTVTDLLGKCLLSPVLAAYQNRSLRVL-----PALDNLSCQAFAPFMSFFGLSSTLQLL 124
Db 56 LAATDGLTSLSPAVFVAYARNSSLGLARGGPA-----LCDAFAPAMTFFGLASMLILF 111
QY 125 AMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFSLAFALFPMGFGKFOYCPGTWCF 184
Db 112 AMAVERCLALSHPLYAQLDGPRCARLALPAIYAFVLCALPLLLGLGHOHQYCPGSMCF 171
QY 185 IQM--VHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTD 242
Db 172 LRMRWAQPGGA-----AFSLAYAGLVALLVAIFLCNCGSVTLSCRMRYQQRHOGS---- 223
QY 243 CAEPRADGREGASPOPL---EELDHLLALLALMTVLFTWCSLPV 281
Db 224 -----LGPRTGDEVDHLLALLALMTVVMVAVCSLP 255

Db 224 -----LGRPRRTGDEVDHLILLALMTVMVAVCSLPL 255

RESULT 13

US-10-225-567A-296

; Sequence 296, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Rough, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 296

; LENGTH: 488

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-296

Query Match 23.7%; Score 364.5; DB 14; Length 488;

Best Local Similarity 31.5%; Pred. No. 1.1e-26;

Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGNASV-MGGVLFSTGLLGNLLALGLLARSGLGWCRRRLRPLPS 59

Db 1 MSTPGVNSASLSPDRLNSPVTIPAVMFIFGVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGTIVTDLGKCLLSPVLAAYAAQNSRLVLPALDNLSCQAFAPFMSFFGLSS 119

Db 53 TFYTLVCGLAUTDLGLTLVSPVTIATYMKGQ-----WPG-QGPLCEYSTFILLFFSLG 106

QY 120 TLQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALPMGFGKVFQYCP 179

Db 107 LSIICAMSVRYLAINHAYFYSHYVDKRLAGLTLFAVYASNVLFALPNMGLGSSRLQYP 166

QY 180 GTWCFTQMVHEGSLSVLGYSVLYSSLMALLVLAIVLNLGAMRNLYAMHRLQHRPSC 239

Db 167 DTWCFTDWT--TNVTAHAAYSMTYAGFSFLILATVLCNVLCGALLRMHROFMERTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----EELDHLLLLALMTVLFVTC 277

Db 225 TEQHHAASVSRGHPAASPALPRLSDFRRRSFRRIAGAEIQWVILLIATSLVLIC 284

QY 278 SLPVIAFV 285

Db 285 SIPLVVRV 292

RESULT 15

US-10-295-027-1326

; Sequence 1326, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynn, Richard

; APPLICANT: Hetezi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714

; LENGTH: 488

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-320-351-3

Query Match 23.7%; Score 364.5; DB 14; Length 488;

Best Local Similarity 31.5%; Pred. No. 1.1e-26;

Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGNASV-MGGVLFSTGLLGNLLALGLLARSGLGWCRRRLRPLPS 59

Db 1 MSTPGVNSASLSPDRLNSPVTIPAVMFIFGVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGTIVTDLGKCLLSPVLAAYAAQNSRLVLPALDNLSCQAFAPFMSFFGLSS 119

Db 53 TFYTLVCGLAUTDLGLTLVSPVTIATYMKGQ-----WPG-QGPLCEYSTFILLFFSLG 106

QY 120 TLQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALPMGFGKVFQYCP 179

Db 107 LSIICAMSVRYLAINHAYFYSHYVDKRLAGLTLFAVYASNVLFALPNMGLGSSRLQYP 166

QY 180 GTWCFTQMVHEGSLSVLGYSVLYSSLMALLVLAIVLNLGAMRNLYAMHRLQHRPSC 239

Db 167 DTWCFTDWT--TNVTAHAAYSMTYAGFSFLILATVLCNVLCGALLRMHROFMERTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----EELDHLLLLALMTVLFVTC 277

Db 225 TEQHHAASVSRGHPAASPALPRLSDFRRRSFRRIAGAEIQWVILLIATSLVLIC 284

QY 278 SLPVIAFV 285

Db 285 SIPLVVRV 292

RESULT 15

US-10-295-027-1326

; Sequence 1326, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynn, Richard

; APPLICANT: Hetezi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714


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; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1326
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1326

Query Match      23.7%; Score 364.5; DB 15; Length 488;
Best Local Similarity 31.5%; Pred.No.1.1e-26;
Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY      1 MKSPFYRCNTTTSVERKNSAV-MGGVLFSTGLGNLLALGLLARSGLWCRRPLRPLPS 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MSTPGVNSSASLSPDLNSPVTIPAVMFIFGVVGNLVAIVLCK-----SRKEQK--ET 52

QY      60 VFYMLVCGLTVTDDLKCLLSPPVLAAYQNRSRLVLPALDNLSCQAPAFPMSPFGLSS 119
      || || || || || || || || || || : : : : : : : : : : : : : :
Db      53 TFYTLVCGLAVTDDLGLLSPVTIATYMKGQ-----WFG-QQPLCEYSTFILLFFSLSG 106

QY      120 TLQLLMALECWLSLGHPEFYRRHITRLGALVAPVVSASFALFCALPEMGFGKFVQYCP 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      107 LSIICAMSVRYLAINHAYFYSHYVDKRLAGLTLFAVYASNVLFCAIPNMGSGSRRLQYP 166

QY      180 GTWCFTIQMVHERGSLSVLGYSVLVSSLMALLVLATVLCNLGAMRNLYAMHRRLQHRPRSC 239
      || || || : : : : : : : : : : : : : : : : : : : : : : : :
Db      167 DTWCFTDWT--TNVTAHAAYSIMYAGFSFLLIATVLCNVLCGALLRMHRQFMRTSLG 224

QY      240 TRD-----CAEPRADGREASPOPL-----BELOHLLLLALMTVLFTWC 277
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      225 TEQHHAASVSRGHPAASPALPRLSDFRRRRSFRRIAGAEIQWVILLIATSLVLVLC 284

QY      278 SLPVIAFY 285
      | : : : : :
Db      285 SLPVVRV 292
```

Search completed: April 22, 2005, 21:43:05
Job time : 154.649 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 20:46:09 ; Search time 14.4611 Seconds
(without alignments)
1969.437 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVGVPKTPGSR 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1467	95.2	359	2	I39153
2	943	61.2	231	2	I59269
3	595.5	38.6	362	2	S66674
4	586	38.0	358	2	I38920
5	585	38.0	358	2	S51312
6	519	33.7	417	2	A54416
7	518.5	33.6	386	2	A57066
8	506.5	32.9	416	2	S52078
9	389	25.2	513	2	A46638
10	383	24.9	488	2	JC2241
11	364.5	23.7	488	2	A53572
12	267	17.3	362	2	A49689
13	267	17.3	366	2	S51280
14	261.5	17.0	361	2	A45211
15	261.5	17.0	364	2	JC2115
16	261.5	17.0	364	2	S65009
17	261.5	17.0	365	2	A44414
18	261.5	17.0	365	2	JN0693
19	251.5	16.3	361	2	A53216
20	251.5	16.3	411	2	B53216
21	250.5	16.3	343	2	A49117
22	250.5	16.3	369	2	A53959
23	250.5	16.3	407	2	T02670
24	244.5	15.9	365	2	I38748
25	244.5	15.9	365	2	S51315
26	244.5	15.9	374	2	I38747
27	244.5	15.9	374	2	S51317
28	244.5	15.9	388	2	S51316
29	244.5	15.9	388	2	I38750

30	244.5	15.9	390	2	S43375
31	244.5	15.9	390	2	S51313
32	244.5	15.9	393	2	S51318
33	244.5	15.9	425	2	S51319
34	239.5	15.5	367	2	JC2056
35	238.5	15.5	362	2	S36766
36	238.5	15.5	385	2	S36765
37	238.5	15.5	387	2	S36767
38	238.5	15.5	417	2	S36764
39	237	15.4	341	2	I55623
40	236.5	15.3	341	2	JH0606
41	219.5	14.2	402	1	A49690
42	209.5	13.6	405	2	S65525
43	197	12.8	366	2	A49877
44	194	12.6	366	2	I53488
45	194	12.6	366	2	S51281

ALIGNMENTS

RESULT 1

I39153
prostanoid DP receptor - human
N:Alternate names: prostaglandin D2 receptor
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence revision 03-May-1996 #text_change 09-Jul-2004
C:Accession: I39153; I39150; I39149
R:Boie, Y.; Sawyer, N.; Slipetz, D.M.; Metters, K.M.; Abramovitz, M.
J. Biol. Chem. 270, 18910-18916, 1995
A:Title: Molecular cloning and characterization of the human prostanoid DP receptor.
A:Reference number: I39149; MUID:95370201; PMID:7642548
A:Accession: I39153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <RE3>
A:Cross-references: UNIPROT:Q13258; EMBL:U31332; NID:G940378; PIDN:AAC50178.1; PID:G940375
A:Accession: I39150
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 216-359 <RE2>
A:Cross-references: EMBL:U31099; NID:G940376; PIDN:AAC50177.1; PID:G940377
A:Accession: I39149
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 283-328 <RE3>
A:Cross-references: EMBL:U31098; NID:G940374; PIDN:AAC50176.1; PID:G940375
C:Genetics: GDB:PTGDR
A:Gene: GDB:PTGDR
A:Cross-references: GDB:681159
A:Map position: 10q23-10q23
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor

Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 9.2e-118;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKSPYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCSSRPLPLPSV	60
Db	1	MKSPYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCSSRPLPLPSV	60
Qy	61	FYMLVCGITVTDLGKCLLSPVVLAAYAQNSRLRVLAAPALDNLSCQAFAFMSFFGLSST	120
Db	61	FYMLVCGITVTDLGKCLLSPVVLAAYAQNSRLRVLAAPALDNLSCQAFAFMSFFGLSST	120
Qy	121	LQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALPMWGKGFVQYCPG	180
Db	121	LQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALPMWGKGFVQYCPG	180
Qy	181	TWCFIQWHEGSGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRPSCST	240
Db	181	TWCFIQWHEGSGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRLQRPSCST	240

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QY 241 RDCARPRADGRASPOPLEELHLLALLMTVLFTWCSPV 282
Db 241 RDCARPRADGRASPOPLEELHLLALLMTVLFTWCSPV 282

RESULT 2
159269
prostaglandin D receptor (prostanoid DP receptor) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Sep-1998
C:Accession: I59269
R:Hitata, M.; Kakizuka, A.; Aizawa, M.; Ushikubi, F.; Narumiya, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 11192-11196, 1994
A:Title: Molecular characterization of a mouse prostaglandin D receptor and functional e
A:Reference number: I59269; MUID:95062232; PMID:7972033
A:Accession: I59269
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-231 <RES>
A:Cross-references: GB:D29764; NID:g577718; PID:g577719
C:Superfamily: prostaglandin E receptor EPI

Query Match 61.2%; Score 943; DB 2; Length 231;
Best Local Similarity 79.2%; Pred. No. 3.2e-73;
Matches 179; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPRLPSPVYMLV 65
Db 5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPRLPSPVYMLV 64

QY 66 CGLTVDLLGKCLSPVLAQAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 65 CGLTVDLLGKCLSPVLAQAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 124

QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 185
Db 125 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 184

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVCNLGNAMRNLYAMHRR 231
Db 185 QMVHBEGLSVGLSVYSSLMALLVLAIVCNLGNAMRNLYAMHRR 230

RESULT 3
S66674
prostaglandin E receptor EP2 subtype - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66674
R:Katayama, M.; Nishigaki, N.; Sugimoto, Y.; Morimoto, K.; Negishi, M.; Narumiya, S.; I
FEBS Lett. 372, 151-156, 1995
A:Title: The mouse prostaglandin E receptor EP(2) subtype: cloning, expression, and Nor
A:Reference number: S66674; MUID:96000196; PMID:7556658
A:Accession: S66674
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <XAT>
A:Cross-references: UNIPROT:Q62053; EMBL:P50589; NID:G829048; PID:BAA09137.1; PID:G8290
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.6%; Score 595.5; DB 2; Length 362;
Best Local Similarity 45.4%; Pred. No. 2.2e-43;
Matches 128; Conservative 50; Mismatches 87; Indels 17; Gaps 7;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 65
Db 14 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 72

QY 66 CGLTVDLLGKCLSPVLAQAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 73 TELVLTDLGLTCLISPPVLAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 130
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QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 185
Db 131 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 190

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVCNLGNAMRNLYAMHRRLQRHPRSCSTRDCAE 245
Db 191 R--HGR-----TAYLQLVATVMTLLIVAVLACNFSVILNIRMHRRSR--SRCGLSGSS 241

QY 246 PRADG---REASPOPLEELHLLALLMTVLFTWCSPVIAF 284
Db 242 LRFGSRRRGERTSMAEETHLLIALLMTITFAICSLPFTIF 283

RESULT 4
138920
prostaglandin E2 receptor - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I38920
R:Regan, J.W.; Bailey, T.J.; Pepperl, D.J.; Pierce, K.L.; Bogardus, A.M.; Donello, J.E.;
Mol. Pharmacol. 46, 213-220, 1994
A:Title: Cloning of a novel human prostaglandin receptor with characteristics of the pha
A:Reference number: I38920; MUID:94359483; PMID:8078484
A:Accession: I38920
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-358 <RES>
A:Cross-references: UNIPROT:P43116; EMBL:U19487; NID:G639719; PID:AAA61681.1; PID:G63262;
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.0%; Score 586; DB 2; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.4e-42;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 65
Db 13 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 71

QY 66 CGLTVDLLGKCLSPVLAQAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 72 TELVLTDLGLTCLISPPVLAQNSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 129

QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 185
Db 130 MALECWLISLGHFFYRRHITLRLGALVAPVSAFSLAFALPFGFKFVQYCPGTWCFI 189

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVCNLGNAMRNLYAMHRRLQRHPRSCSTRDCAE 245
Db 190 R--HGR-----TAYLQLVATVMTLLIVAVLACNFSVILNIRMHRRSR--SRCGLSGSS 240

QY 246 ---PRADGRASPOPLEELHLLALLMTVLFTWCSPVIAF 284
Db 241 GRGFGARRRGERTSMAEETHLLIALLMTITFAICSLPFTIF 283

RESULT 5
S51312
EP2 prostaglandin receptor - human
C:Species: Homo sapiens (man)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51312
R:Oakley, C.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: S51312
A:Accession: S51312
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <OAK>
A:Cross-references: UNIPROT:P43116; EMBL:X83868; NID:G633205; PID:CAA58749.1; PID:G63320
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.0%; Score 585; DB 2; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.7e-42;
```


Biochim. Biophys. Acta 1224, 601-605, 1994
A:Title: Cloning and expression of a cDNA for rat prostacyclin receptor.
A:Reference number: S52078; MUID:95101758; PMID:7803522

A:Accession: S52078
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SAS>
A:Cross-references: UNIPROT:P43253; GB:D28966; NID:G602775; PID:BAA06091.1; PID:G602776
C:Superfamily: prostaglandin E receptor EPI

Query Match 32.9%; Score 506.5; DB 2; Length 416;
Best Local Similarity 43.6%; Pred. No. 9.9e-36;
Matches 120; Conservative 38; Mismatches 92; Indels 25; Gaps 7;

QY 8 CONTTSVEKGNNAVWGVLFTSLGNLALGLLARSGLWCSSRRPLRLPLSPVFMVLCG 67

DB 34 CWNITVQDSVGPATSTLMFVAGVGVNGLALGILG-----ARR--RSHPSAFVAVLVG 84

QY 68 LTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLAMA 127

DB 85 LAVTDLLGTCFLSPAVFVAYARNSLLGLAHG-GTWMLCDTFAFAMTFFGLASTLILFAMA 143

QY 128 LECWLSLGHFPYRRHITLRLGALVAPVVSFSLAFALCFPMGFGKFQVQCPGTWCFTQM 187

DB 144 VERCLALSHPLYAQLDGPRCARLALPAIYAFCLFCSLPLGLGHEHQYCPGSCWCFIRM 203

QY 188 -VHEGSLSVLGYSVLYSSLSMALLVTLVCLNGLAMRNLYAMHRLQHRPRSTRDCAEP 246

DB 204 RSPQPGGCA---FSLAYASLMALLVTSIFFCNGSVTLSLCHMYRQRRHGSFV-----P 255

QY 247 RADGREASQPQLEEDHLLALMTVLTWCMSLPV 281

DB 256 TSRARE-----DEVHLLILALMTGIMAVCSLPL 284

RESULT 9

A46638
prostaglandin E receptor EP2 subtype - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A46638
R:Honda, A.; Sugimoto, Y.; Namba, T.; Watabe, A.; Irie, A.; Negishi, M.; Narumiya, S.; I
J. Biol. Chem. 268, 7759-7762, 1993

A:Title: Cloning and expression of a cDNA for mouse prostaglandin E receptor EP2 subtype

A:Reference number: A46638; MUID:93216741; PMID:8385118

A:Accession: A46638

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-513 <HON>

A:Cross-references: UNIPROT:P32240; GB:D13458; NID:G303699; PID:BAA02714.1; PID:G303700

A:Experimental source: mastocytoma P-815 cells

A>Note: sequence extracted from NCBI backbone (NCBIN:128997, NCBI:P:128998)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 25.2%; Score 389; DB 2; Length 513;
Best Local Similarity 31.5%; Pred. No. 1.3e-25;
Matches 99; Conservative 57; Mismatches 110; Indels 48; Gaps 9;

QY 1 MKSPFYRCQNTTSVEKGNNAV-MGGVLFSTGLGNLALGLLARSGLWCSSRRPLRLPLPS 59

DB 26 MSIPGVNASFSSTPERLNSPVTIPAVMFIFGVVGNLVAIVLCK-----SRKEQK--ET 77

QY 60 VFYMLVCGLTVTDDLKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSS 119

DB 78 TFYTLVCGGLAVTDLLGLTLLVSPVTIATYMKGO-----WFG-DQALCDYSTFILLFFGLSG 131

QY 120 TLQLLMALECWLSLGHFPFYRRHITLRLGALVAPVVSFSLAFALCFPMGFGKFVQYCP 179

DB 132 LSIICAMSIERYLAINHAYFYSHYVDKRLAGLTFLFAIYASNVLFCAIPNMGGRSERQVP 191

QY 180 GTWCFTQMVHEBGLSVLGY---SVLYSSLMALLVTLVCLNGLAMRNLYAMHRLQHR-- 234

DB 192 GTWCFTI-----DWTNTVTAYAAFSYMYAGFSFLILATVLCNVLCGALLRMHROFMRT 246

QY 235 -----HPRSCTRDCAEPADGREASPOPLE-----ELDHLLILLALMT 271

DB 247 SLGTEQHHAAAAAASVACRHHAGASPALQRLSDFRRRSRPRRIAGAEIQMVILLIATS 306

QY 272 VLFTWCMSLPVIAFV 285

DB 307 LVVLICSIPLVVVR 320

RESULT 10

JC2241
prostaglandin E receptor EP2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: JC2241

A:Sando, T.; Usui, T.; Tanaka, I.; Mori, K.; Sasaki, Y.; Fukuda, Y.; Namba, T.; Sugimoto,

Biochem. Biophys. Res. Commun. 200, 1329-1333, 1994

A:Title: Molecular cloning and expression of rat prostaglandin E receptor EP2 subtype.

A:Reference number: JC2241; MUID:94241990; PMID:8185583

A:Accession: JC2241

A:Molecule type: mRNA

A:Residues: 1-488 <SAS>

A:Cross-references: UNIPROT:P43114; DDBJ:D28860; NID:G516827; PIDN:BAA06011.1; PID:G51682

A:Experimental source: lung

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:20-44/Domain: transmembrane #status predicted <TM1>

F:56-79/Domain: transmembrane #status predicted <TM2>

F:97-116/Domain: transmembrane #status predicted <TM3>

F:136-160/Domain: transmembrane #status predicted <TM4>

F:185-211/Domain: transmembrane #status predicted <TM5>

F:271-298/Domain: transmembrane #status predicted <TM6>

F:316-335/Domain: transmembrane #status predicted <TM7>

F:7,177/Binding site: carboxylate (Asn) (covalent) #status predicted

F:222,262,373,374/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #st

Query Match 24.9%; Score 383; DB 2; Length 488;
Best Local Similarity 32.5%; Pred. No. 4e-25;
Matches 102; Conservative 58; Mismatches 106; Indels 48; Gaps 11;

QY 1 MKSPFYRCQNTTSVEKGNNAV-MGGVLFSTGLGNLALGLLARSGLWCSSRRPLRLPLPS 59

DB 1 MSIPGVNASFSSTPERLNSPVTIPAVMFIFGVVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGLTVTDDLKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSS 119

DB 53 TFYTLVCGGLAVTDLLGLTLLVSPVTIATYMKGO-----WFG-DQALCDYSTFILLFFGLSG 106

QY 120 TLQLLMALECWLSLGHFPFYRRHITLRLGALVAPVVSFSLAFALCFPMGFGKFVQYCP 179

DB 107 LSIICAMSIERYLAINHAYFYSHYVDKRLAGLTFLFAIYASNVLFCAIPNMGGRSERQVP 166

QY 180 GTWCFTQMVHEBGLSVLGY---SVLYSSLMALLVTLVCLNGLAMRNLYAMHRLQHR- 231

DB 167 GTWCFTI-----DWTNTVTAYAAFSYMYAGFSFLILATVLCNVLCGALLRMHROFMRT 221

QY 232 ---LQHRPRSTRDCAEPADGREASPOPLE-----ELDHLLILLALMT 271

DB 222 SLGTEQHHAAAAAASVACRHHAGASPALQRLSDFRRRSRPRRIAGAEIQMVILLIATS 281

QY 272 VLFTWCMSLPVIAFV 285

DB 282 LVVLICSIPLVVVR 295

RESULT 11

A53572
prostaglandin E2 receptor EP2 subtype - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: A53572; 152289

R:Bastien, L.; Sawyer, N.; Grygorczyk, R.; Metters, K.M.; Adam, M.
 J. Biol. Chem. 269, 11873-11877, 1994
 A:Title: Cloning, functional expression, and characterization of the human prostaglandin
 A:Reference number: A53572; MUID:94216291; PMID:8163486
 A:Accession: A53572
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-488 <BAS>
 R:An, S.; Yang, J.; Xia, M.; Goetzl, E.J.
 Biochem. Biophys. Res. Commun. 197, 263-270, 1993
 A:Title: Cloning and expression of the EP2-subtype of human receptors for prostaglandin
 A:Reference number: I52289; MUID:94071953; PMID:8250933
 A:Accession: I52289
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-463, 'WAC', 467-488 <ANS>
 A:Cross-references: GB:L25124; NID:9435049; PIDN:AAA36438.1; PID:9435050
 C:Genetics: EP2
 A:Gene: GDB:PTGER2; EP2
 A:Cross-references: GDB:270672; OMIM:176804
 A:Map position: 5p13.1-5p13.1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.7%; Score 364.5; DB 2; Length 488;
 Best Local Similarity 31.5%; Pred. No. 1.5e-23;
 Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGNASV-MGGVLFSTGLGNLLALGLLARSGLGWCRRPLPLPS 59
 DB 1 MSTPGVNSASLPDRINSPTIPAVMFIFGVGNLVAVLVLC-----SRKEQK--ET 52

QY 60 VFYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFPMFSGFLGS 119
 DB 53 TYTTLVCGLAIVDGLTLVSPVTIYMKGQ-----WFG-GQPLCEYTFILLFSLSG 106

QY 120 TLQLLMALECLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALPMFGKFGVQYCP 179
 DB 107 LSIICAMSVRYLAINHAFYSHYVDKRLAGLTLFPAVYASNVLFALPKNGLGSSRLQYP 166

QY 180 GTWCTIQVHEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPRSC 239
 DB 167 DTWCFIDMT--TNVTAHAAYSYNYAGFSFLILATVLCNVLGALLRHQFMRTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----BELDHLILLALMTVLTFC 277
 DB 225 TQHHAAAAASVASRCHPAASPALPRLSDFRRRSRFRRTAGAEIQNVILLIATSLVVLIC 284

QY 278 SLPVIAFV 285
 DB 285 SIPLVVRV 292

RESULT 12
 S48689
 prostaglandin E(2) receptor (EP3 beta subtype) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S48689; S46934
 R:Neuschaefer-Rube, F.; DeVries, C.; Haenecke, K.; Jungermann, K.; Pieschel, G.P.
 FEBS Lett. 351, 119-122, 1994
 A:Title: Molecular cloning and expression of a prostaglandin E(2) receptor of the EP(3-
 A:Reference number: S48689; MUID:94357264; PMID:8076679
 A:Accession: S48689
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-362 <NEU>
 A:Cross-references: EMBL:X80133; NID:G514418; PIDN:CAA56432.1; PID:G514419
 C:Superfamily: prostaglandin E receptor EPI

Query Match 17.3%; Score 267; DB 2; Length 362;
 Best Local Similarity 29.5%; Pred. No. 2.4e-15;

Matches 85; Conservative 45; Mismatches 116; Indels 42; Gaps 9;

QY 10 NTTTSVEKGNASVAMGG---VLFSTGLGNLLALGLLARSGLGWCRRPLPLPSVFYMLVC 66
 DB 16 NQSSAADGCGSVSVAPPITMVTGFGVGNALMALLVSR-----YRRRESKRKKSFLLCIG 70

QY 67 GLUTVDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFPMFSGFLGSSTLQLLAM 126
 DB 71 WLALTDLVGQLLTSPVILVLSQRRWEQDPS--GRLCCTFFGLTMTVFLGSLSLVASAM 128

QY 127 ALECMWLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALPMFGKFGVQYCPGTWCFFI- 185
 DB 129 AVERALATRAPHWYASHMKTRATRVLLGVWLSVLAFLALLPVLGVRYSVQWPGTWCFFIS 188

QY 186 -----QMVEEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPR 237
 DB 189 TGPAGNETDSAREPGSVA---FASAFACLGILLALVVTACNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASPOPLEELDHLLALLMTVLTFCWCSLPVI 282
 DB 236 RCRAKAAASQSSAOWGRITTTETAIQ-----LMGIMCVL-SVCWSPLL 276

RESULT 13
 S51280
 EP3-alpha receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 23-Jul-1999
 C:Accession: S51280
 R:Neuschaefer-Rube, F.; de Vries, C.; Haenecke, K.; Jungermann, K.; Pieschel, G.P.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S51280
 A:Accession: S51280
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-366 <NEU>
 A:Cross-references: EMBL:X83855; NID:G633623; PIDN:CAA58735.1; PID:G633624
 C:Superfamily: prostaglandin E receptor EPI

Query Match 17.3%; Score 267; DB 2; Length 366;
 Best Local Similarity 29.5%; Pred. No. 2.4e-15;
 Matches 85; Conservative 45; Mismatches 116; Indels 42; Gaps 9;

QY 10 NTTTSVEKGNASVAMGG---VLFSTGLGNLLALGLLARSGLGWCRRPLPLPSVFYMLVC 66
 DB 16 NQSSAADGCGSVSVAPPITMVTGFGVGNALMALLVSR-----YRRRESKRKKSFLLCIG 70

QY 67 GLUTVDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFPMFSGFLGSSTLQLLAM 126
 DB 71 WLALTDLVGQLLTSPVILVLSQRRWEQDPS--GRLCCTFFGLTMTVFLGSLSLVASAM 128

QY 127 ALECMWLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALPMFGKFGVQYCPGTWCFFI- 185
 DB 129 AVERALATRAPHWYASHMKTRATRVLLGVWLSVLAFLALLPVLGVRYSVQWPGTWCFFIS 188

QY 186 -----QMVEEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPR 237
 DB 189 TGPAGNETDSAREPGSVA---FASAFACLGILLALVVTACNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASPOPLEELDHLLALLMTVLTFCWCSLPVI 282
 DB 236 RCRAKAAASQSSAOWGRITTTETAIQ-----LMGIMCVL-SVCWSPLL 276

RESULT 14
 A45211
 prostaglandin E receptor EP3 beta, PGE receptor EP3 beta (alternatively spliced) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A45211
 R: Sugimoto, Y.; Negishi, M.; Hayashi, Y.; Namba, T.; Honda, A.; Watabe, A.; Hirata, M.; I
 J. Biol. Chem. 268, 2712-2716, 1993
 A:Title: Two isoforms of the EP3 receptor with different carboxyl-terminal domains. Ident

A;Reference number: A45211; MUID:93155085; PMID:8381413

A;Accession: A45211

A;Status: Preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-361 <SUP>

A;Cross-references: UNIPROT:P30557; GB:D13321; NID:G286108; PIDN:BA02578.1; PID:G286109

A;Experimental source: mastocytoma P-815

A;Note: sequence extracted from NCBI backbone (NCBIP:124180)

C;Superfamily: prostaglandin E receptor EPI

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.0%; Score 261.5; DB 2; Length 361;

Best Local Similarity 29.4%; Pred. No. 7e-15;

Matches 85; Conservative 50; Mismatches 107; Indels 47; Gaps 11;

QY 10 NNTSVEKGNVAVGGV-LFSTGLLGNLLALGLLARSGLWCRRRLPLPSVFMVLCGL 68

DB 18 SSTTDCGVSVAFFITMTVTGFGNALAMLLVRS-----YRRRESKRKKSFLLCIGWL 72

QY 69 TTTDLGKCLLSPVVLAAVAQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAMAL 128

DB 73 AUTDLVGQLTSPVILVYLSORRWEQLDPS--GRLCFTFGLTMTVFGLSLLVASAMAV 130

QY 129 ECWLSLGHFFFYRRHITLRLGALVAVP---VSAFSLAFALCFPMGFGKVFQYCPGTWCFFI 185

DB 131 ERALAIRAPHWYASHMKTR---ATPVLGGVWLSVLAFALLPVLGVGRYSVQWPGTWCFFI 186

QY 186 QM-----VHEGSLSVLGYSVLSMALLVLATVLCNLGAMRNLYAMHRRLLQRHP 236

DB 187 STGPAGNETDPAREPGSVA---FASAFACLGILALVTFACNLATIKALVS----- 234

QY 237 RSCTRDCAEPRAD---GREASQPQLLELDHLLALLMTVLTMCSLPVI 282

DB 235 -RCRAKAASQSSAQWGRITTTETAIO-----LMGIMCVL-SVCWSPLL 275

RESULT 15

JC2115

Prostaglandin E receptor EP3 subtype rEP3B - rat

N;Contains: prostaglandin E receptor rEP3A

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

C;Accession: JC2115

R;Takeuchi, K.; Takahashi, N.; Abe, T.; Abe, K.

Biochem. Biophys. Res. Commun. 199; 834-840, 1994

A;Title: Two isoforms of the rat kidney EP3 receptor derived by alternative RNA splicing

A;Reference number: JC2115; MUID:94183265; PMID:8135830

A;Accession: JC2115

A;Molecule type: mRNA

A;Residues: 1-364 <TAK>

A;Note: the authors translated the codon GAT for residue 360 as Val

C;Comment: this protein is co-localized to distal tubules exerting an effect on water an

C;Superfamily: prostaglandin E receptor EPI

C;Keywords: glycoprotein; GTP binding; phosphoprotein; receptor; transmembrane protein

F;1-364/Product: prostaglandin E receptor rEP3B #status predicted <PEC>

F;1-335/Product: prostaglandin E receptor rEP3A #status predicted <PER>

F;31-55/Domain: transmembrane #status predicted <TM1>

F;69-89/Domain: transmembrane #status predicted <TM2>

F;108-130/Domain: transmembrane #status predicted <TM3>

F;152-173/Domain: transmembrane #status predicted <TM4>

F;204-229/Domain: transmembrane #status predicted <TM5>

F;260-283/Domain: transmembrane #status predicted <TM6>

F;304-325/Domain: transmembrane #status predicted <TM7>

F;16193/Binding site: carbonyl (Asn) (covalent) #status predicted

F;59.64/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pred

Query Match

Best Local Similarity 17.0%; Score 261.5; DB 2; Length 364;

Matches 86; Conservative 44; Mismatches 112; Indels 49; Gaps 11;

QY 10 NNTSVEKGNVAVGGV---VLFSTGLLGNLLALGLLARSGLWCRRRLPLPSVFMVLCV 66

DB 16 NQSSAADCGSVSAFFITMTVTGFGNALAMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKCLLSPVVLAAVAQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAM 126

DB 71 WLAITDLVGQLTSPVILVYLSORRWEQLDPS--GRLCFTFGLTMTVFGLSLLVASAM 128

QY 127 ALECWLSLGHFFFYRRHITLRLGALVAVP---VSAFSLAFALCFPMGFGKVFQYCPGTWC 183

DB 129 AVERALAIRAPHWYASHMKTR---ATPVLGGVWLSVLAFALLPVLGVGRYSVQWPGTWC 184

QY 184 FI-----QMWHEGSLSVLGYSVLSMALLVLATVLCNLGAMRNLYAMHRRLLQR 234

DB 185 FISTGPAGNETDSAREPGSVA---FASAFACLGILALVTFACNLATIKALVS----- 234

QY 235 HPRSCTRDCAEPRAD---GREASQPQLLELDHLLALLMTVLTMCSLPVI 282

DB 235 ---RCRAKAASQSSAQWGRITTTETAIO-----LMGIMCVL-SVCWSPLL 275

Search completed: April 22, 2005, 21:30:02

Job time : 15.4611 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 18:00:17 ; Search time 52.4214 Seconds
(without alignments)
2891.482 Million cell updates/sec

Title: US-10-689-861-2

Perfect score: 1541

Sequence: 1 MKSPYRCQNTTSVKGNSA.....CSLPVIAFVGVPKTPGSR 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1467	95.2	359	1	PD2R_HUMAN	Q13258 homo sapien
2	1127	73.1	357	2	Q9R261	Q9R261 rattus norv
3	1125	73.0	357	2	O35932	O35932 rattus norv
4	1100	71.4	357	1	PD2R_MOUSE	P70262 mus musculus
5	1095	71.1	357	2	O8CCM3	O8CCM3 mus musculus
6	802	39.1	361	1	PE22_CANFA	Q9X822 canis famil
7	595.5	38.6	362	1	PE22_MOUSE	Q62053 mus musculus
8	593.5	38.5	308	2	Q8B275	Q8B275 mus musculus
9	585	38.0	358	1	PE22_HUMAN	P43116 homo sapien
10	569	36.9	361	2	Q8HY57	Q8HY57 oryctolagus
11	569	36.9	371	2	Q6NZ15	Q6NZ15 xenopus lae
12	565.5	36.7	357	1	PE22_RAT	Q62928 rattus norv
13	556	36.1	352	2	Q8MJ09	Q8MJ09 bos taurus
14	549	35.6	385	1	PI2R_BOVIN	P73993 bos taurus
15	519	33.7	415	1	PI2R_MOUSE	P43252 mus musculus
16	518.5	33.6	386	1	PI2R_HUMAN	P43119 homo sapien
17	506.5	32.9	416	1	PI2R_RAT	P43253 rattus norv
18	493.5	32.0	281	2	Q6PFT8	Q6PFT8 brachydanio
19	393	25.5	292	2	Q7TSX4	Q7TSX4 rattus norv
20	389	25.2	488	2	Q91VE4	Q91VE4 mus musculus
21	389	25.2	513	1	PE24_MOUSE	P32240 mus musculus
22	383	24.9	488	1	PE24_RAT	P43114 rattus norv
23	372.5	24.2	492	2	Q9TUL6	Q9TUL6 canis famil
24	372	24.1	492	2	Q8MJ08	Q8MJ08 bos taurus
25	364.5	23.7	488	1	PE24_HUMAN	P35408 homo sapien
26	363.5	23.6	490	2	Q95J39	Q95J39 macaca fasc
27	363.5	23.6	490	2	P7JGJ7	P7JGJ7 papio hamad
28	363	23.6	488	1	PE24_RABIT	Q28691 oryctolagus
29	361.5	23.5	490	1	PE24_PANTR	Q95K20 pan troglod
30	316.5	20.5	154	2	Q7TSX3	Q7TSX3 mus musculus
31	300.5	19.5	168	2	Q95M50	Q95M50 bos taurus

32	277.5	18.0	133	2	Q95M51	Q95M51 bos taurus
33	266	17.3	362	2	Q6PDF2	Q6PDF2 mus musculus
34	261.5	17.0	360	2	Q99PG3	Q99PG3 rattus norv
35	261.5	17.0	365	1	PE23_MOUSE	P30557 mus musculus
36	261.5	17.0	365	1	PE23_RAT	P34980 rattus norv
37	255.5	16.6	370	2	Q6VPS4	Q6VPS4 canis famil
38	255.5	16.6	416	2	Q6VPS5	Q6VPS5 canis famil
39	251.5	16.3	411	1	PE23_RABIT	P46069 oryctolagus
40	250.5	16.3	369	1	TA2R_HUMAN	P21731 homo sapien
41	250.5	16.3	407	2	O75228	O75228 homo sapien
42	244.5	15.9	366	2	Q6TTN3	Q6TTN3 homo sapien
43	244.5	15.9	390	1	PE23_HUMAN	P43115 homo sapien
44	244.5	15.9	393	2	O00326	O00326 homo sapien
45	244.5	15.9	402	2	O00325	O00325 homo sapien

ALIGNMENTS

RESULT 1

PD2R_HUMAN STANDARD; PRT; 359 AA.
AC Q13258; Q13250; Q13251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
GN Name=PTGDR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370201; PubMed=7642548; DOI=10.1074/jbc.270.32.18910;
RA Boie Y., Sawyer N., Slipetz D.M., Metters K.M., Abramovitz M.;
RT "Molecular cloning and characterization of the human prostanoid DP receptor."
RL J. Biol. Chem. 270:18910-18916 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of this receptor is mainly mediated by G(s) proteins that stimulate adenylyate cyclase, resulting in an elevation of intracellular cAMP. A mobilization of calcium is also observed, but without formation of inositol 1,4,5-trisphosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in retina and small intestine.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Retina;
RX MEDLINE=98387174; PubMed=9721719; Kanaoka Y., Eguchi N., Gordon W.C.,
RA Gershenko D., Beuckmann C.T., Kanaoka Y., Eguchi N., Gordon W.C.,
RA Urade Y., Bazan N.G., Hayaishi O.;
RT "Dominant expression of rat prostanoic DP receptor mRNA in
RT leptomeninges, inner segments of photoreceptor cells, iris epithelium,
RT and ciliary processes."
RL J. Neurochem. 71:937-945(1998).
DR EMBL; U92289; AAB71762.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004956; F:prostaglandin D receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR000376; GPCR Rhodopsin.
DR InterPro; IPR008365; Prostanoidrecept.
DR InterPro; IPR001105; Thbox_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1788; PROSTANOIDR.
DR PRINTS; PRO0854; PRSTNOIDDR.
DR PRINTS; PRO0429; THROMBOXANER.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 357 AA; 39802 MW; DB966276DD68184C CRC64;

Query Match 73.0%; Score 1125; DB 2; Length 357;
Best Local Similarity 78.0%; Pred. No. 7.6e-80;
Matches 216; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWSRRRLPLPSVPMVLV 65
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWSRRRLPLPSVPMVLV 64
QY 66 CGLTVDLLGKCLSPVLAAYQNRSLRVLAAPALDNSLCOAFAPFMSFGLSSTLQLLA 125
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 CGLTVDLLGKCLSPVLAAYQNRSLRVLAAPALDNSLCOAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHFFFYRRHITLRLGALVAPVSAFSLAFALCFALPMGKGVQYCPGTWCFI 185
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 MALECWLSLGHFFFYRRHITLRLGALVAPVSAFSLAFALCFALPMGKGVQYCPGTWCFI 184
QY 186 QMVBEGSLVGLVYSSLMALLVATVLCNLGMRNLYAMHRRQLQRHPSCTRDCAE 245
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 QMVBEGSLVGLVYSSLMALLVATVLCNLGMRNLYAMHRRQLQRHPSCTRDCAE 244
QY 246 PRADGREGASPOPLELDHLLALMTVLTMCSLPVI 282
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 SGSDYRHGSPNPLELDHFLVLLATVLTMCSLPVI 281

RESULT 4
PD2R MOUSE
ID PD2R MOUSE STANDARD; PRT; 357 AA.
AC P70263;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
GN Name=Ptdr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Lung;

```

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RX MEDLINE=95062232; PubMed=7972033;
RA Hirata M., Kakizuka A., Aizawa M., Ushikubi F., Narumiya S.;
RT "Molecular characterization of a mouse prostaglandin D receptor and
RT functional expression of the cloned gene."
RL Proc. Natl. Acad. Sci. U.S.A. 91:11192-11196(1994).
CC -!- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
CC this receptor is mainly mediated by G(s) proteins that stimulate
CC adenylyl cyclase, resulting in an elevation of intracellular
CC CAMP. A mobilization of calcium is also observed, but without
CC formation of inositol 1,4,5-trisphosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Most abundantly expressed in the ileum,
CC followed by lung, stomach and uterus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch)
CC
DR EMBL; D29765; BAA06168.1; -.
DR EMBL; D29764; BAA06168.1; JOINED.
DR MGD; MGI:102966; Ptdgr.
DR GO; GO:0004956; F:prostaglandin D receptor activity; IEA.
DR GO; GO:0001785; F:prostaglandin J receptor activity; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR000376; GPCR Rhodopsin.
DR InterPro; IPR008365; Prostanoidrecept.
DR InterPro; IPR001105; Thbox_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1788; PROSTANOIDR.
DR PRINTS; PRO0429; THROMBOXANER.
DR PROSITE; PS00437; G_PROTEIN_RECEP_FL_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 20 Extracellular (Potential).
FT TRANSMEM 21 41 1 (Potential).
FT DOMAIN 42 58 Cytoplasmic (Potential).
FT TRANSMEM 59 79 2 (Potential).
FT DOMAIN 80 106 Extracellular (Potential).
FT TRANSMEM 107 127 3 (Potential).
FT DOMAIN 128 149 Cytoplasmic (Potential).
FT TRANSMEM 150 170 4 (Potential).
FT DOMAIN 171 194 Extracellular (Potential).
FT TRANSMEM 195 215 5 (Potential).
FT DOMAIN 216 261 Cytoplasmic (Potential).
FT TRANSMEM 262 282 6 (Potential).
FT DOMAIN 283 306 Extracellular (Potential).
FT TRANSMEM 307 337 7 (Potential).
FT DOMAIN 338 357 Cytoplasmic (Potential).
FT DISULFID 104 182 By similarity.
FT CARBOHYD 2 2 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 357 AA; 40005 MW; 91CBFF7A5936EB05 CRC64;

Query Match 71.4%; Score 1100; DB 1; Length 357;
Best Local Similarity 75.8%; Pred. No. 6.8e-78;
Matches 210; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWSRRRLPLPSVPMVLV 65
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWSRRRLPLPSVPMVLV 64
QY 66 CGLTVDLLGKCLSPVLAAYQNRSLRVLAAPALDNSLCOAFAPFMSFGLSSTLQLLA 125
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 CGLTVDLLGKCLSPVLAAYQNRSLRVLAAPALDNSLCOAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHFFFYRRHITLRLGALVAPVSAFSLAFALCFALPMGKGVQYCPGTWCFI 185
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 MALECWLSLGHFFFYRRHITLRLGALVAPVSAFSLAFALCFALPMGKGVQYCPGTWCFI 184

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QY 186 OMVHEEGSLVGLYSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRHPSCTRDCAE 245
DB 195 QMIHKERSFVIGFVLSLSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRHPSCTRDCAE 244
QY 246 PRADGREALPOPLELDHLLALLMTVLTFTWCSLPVI 282
DB 245 SGSDYRHGSLHPLLELDHFLVLLATVLTFTWCSLPVI 281

RESULT 5
ID Q8CCM3 PRELIMINARY; PRT; 357 AA.
AC Q8CCM3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:643056C09 product:prostaglandin D receptor,
DE full insert sequence.
GN Name=Ptdgr;
OS Eus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Tahii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1157-1171(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno T., Hanaqaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK032488; BAC27895.1; -.
DR MGD; MGI:102966; Ptdgr.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004956; F:prostaglandin D receptor activity; IDA.
DR GO; GO:0001785; F:prostaglandin J receptor activity; IDA.
DR InterPro; IPR000376; GPCR_Rhodpsn.
DR InterPro; IPR008365; Prostanoidrecept.
DR InterPro; IPR001105; Tbox_receptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01788; PROSTANOIDR.
DR PRINTS; PR00854; PRSTNOIDDP.
DR PRINTS; PR00429; THROMBOXANER.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 357 AA; 39990 MW; A0FAPE3E5D77E952 CRC64;

Query Match 71.1%; Score 1095; DB 2; Length 357;
Best Local Similarity 75.5%; Pred. No. 1.7e-77;
Matches 209; Conservative 26; Mismatches 42; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKGNVGMGVLFSTCLLCNLALGLIARSLGRCRRRLPSPVYVYLV 65
DB 5 YRCQNTTSVEKGNVGMGVLFSTCLLCNLALGLIARSLGRCRRRLPSPVYVYLV 64
QY 66 CGLTVDTLLGKCLSPVLAAYAAQNRSLRVLPALDNLSCQAFAPFMSFFGLSLTQLLIA 125
DB 65 CGLTVDTLLGKCLSPVLAAYAAQNRSLRVLPALDNLSCQAFAPFMSFFGLSLTQLLIA 124
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSASFALCALPFMGFGKVFQVCPGTWCPI 185
DB 125 MALECWLSLGHPPFYRRHITLRLGALVAPVVSASFALCALPFMGFGKVFQVCPGTWCPI 184
QY 186 QMWHEEGSLVGLYSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRHPSCTRDCAE 245
DB 185 QMWHEEGSLVGLYSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRHPSCTRDCAE 244

QY 246 PRADGREALPOPLELDHLLALLMTVLTFTWCSLPVI 282
DB 245 SGSDYRHGSLHPLLELDHFLVLLATVLTFTWCSLPVI 281

RESULT 6
ID PE22 CANFA STANDARD; PRT; 361 AA.
AC Q9XT82;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
DE receptor, EP2 subtype).
GN Name=PTGER2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99338573; PubMed=10410384; DOI=10.1016/S0090-6980(98)00081-1;
RA Hibbs T.A., Lu B., Smock S.L., Vestergaard P., Pan L.C., Owen T.A.;
RT "Molecular cloning and characterization of the canine prostaglandin E
```


126 M ALECWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGKFKVQYCPGTWCFI 185
 130 M ALEWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGKFKVQYCPGTWCFI 189
 186 QMVHEGSLVGLSYSLMALVATVLCNLGAMRNLYAMHRLQRPSCRTDCAE 245
 190 R--HGR-----TAYLQLYATALLLIVSVLACNFSVILNIRHRSRR--SRCGPSLGS 240
 246 ----PRAGREASPOPLELHLLALMTVLTWCSPVIAF 284
 241 CRGGCARRRRGERSVMAEETHLLIIMTITFAVCSLPFTTF 283

RESULT 10
 Q8HY57
 ID Q8HY57 PRELIMINARY; PRT; 361 AA.
 AC Q8HY57;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Prostaglandin E2 receptor EP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Breyer M.D.;
 RT "Cloning of rabbit prostaglandin E2 receptor EP2.";
 RL J. Am. Soc. Nephrol. 7:1646-1646(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=12037143; DOI=10.1186/1471-2210-2-14;
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Redha R., Breyer R.M., Breyer M.D.;
 RT "Cloning and expression of the rabbit prostaglandin EP2 receptor.";
 RL BMC Pharmacol. 2:14-14(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY166779; AA013013.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR001923; EP2 receptor.
 DR InterPro; IPR000276; GPCR Rhodopsin.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRRHODOPSIN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 361 AA; 39945 MW; E735BC61F60B1D9D CRC64;

Query Match 36.9%; Score 569; DB 2; Length 361;
 Best Local Similarity 43.9%; Pred. No. 28-36;
 Matches 126; Conservative 41; Mismatches 94; Indels 26; Gaps 7;
 8 CQNTSVKGNAGVGVGFSTGLGNLALGLLARSGLGWCSSRRPLRPLP-SVFVMLVC 66
 13 CSTRQWLPSEGSFATSAVNFSGVGLNLIALLARRWRADGRSAGRTSLSLFVLVT 72
 67 GLTVTDLLGKLLSPVLLAAYANQSLRVLAPALDNSLCOAFPMWFFGLSSTLQLLAM 126
 73 ELVFTDLLGCTFISPVLLASVARNOTLVALEP--DGRACTYFAFANTFFSLATMLMLFAM 130

127 ALECWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGKFKVQYCPGTWCFI 186
 131 ALEWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGKFKVQYCPGTWCFI 190
 187 QMVHEGSLVGLSYSLMALVATVLCNLGAMRNLYAMHRLQRPSCRTDCAE 246
 191 --HGR-----TAYLQLYATALLLIVSVLACNLSVICNLVHMYRRARR-----SRCGPS 237
 247 RADGREASP-----OPTLELDHLLALMTVLTWCSPVIAF 284
 238 SCGSR--GGTGRRRGERSVMAEETHLLIIMTITFAVCSLPFTTF 283

RESULT 11
 Q6NZ15
 ID Q6NZ15 PRELIMINARY; PRT; 371 AA.
 AC Q6NZ15;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MGC69060 protein.
 GN Name=MGC69060;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schen J.E.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC066120; AAH66120.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR001923; EP2_receptor.


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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE EP2 receptor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22694625; PubMed=12810564; DOI=10.1210/en.2002-0088;
RA Arsh J.A., Banu S.K., Chapdelaine P., Emond V., Kim J.J.,
RA MacLaren L.A., Fortier M.A.;
RT "Molecular Cloning and Characterization of Bovine Prostaglandin E(2)
RT Receptors EP2 and EP4: Expression and Regulation in Endometrium and
RT Myometrium during the Estrous Cycle and Early Pregnancy.";
RL Endocrinology 144:3076-3091(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF539402; AAN01234.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR001923; EP2 receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR008365; Prostanoidrecept.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PRINTS: PR01788; PROSTANOIDR.
DR PRINTS: PR00581; PRSTNOIDEP2R.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_3; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 39726 MW; 9BB8FBF445B37287 CRC64;

Query Match 36.1%; Score 556; DB 2; Length 352;
Best Local Similarity 45.0%; Pred. No. 2e-35;
Matches 121; Conservative 46; Mismatches 88; Indels 14; Gaps 5;

Qy 17 GNSAVMGVLFSTGLGNLLALGLARSLGWCRRRLPLP-SVFYMLVGLTDTLLG 75
Dy 17 GNSAVMGVLFSTGLGNLLALGLARSLGWCRRRLPLP-SVFYMLVGLTDTLLG 75
Dy 22 GSPAISSVMFTAGVLEGNLIALAVRRWGRSGRSGNSLSLHVLTDLTLLG 81
Qy 76 KLLSPVVLAAAYQNRSLRVAPALDNLSCQAFPAFFSFGLSSTLQLLAMALECWL 135
Dy 76 KLLSPVVLAAAYQNRSLRVAPALDNLSCQAFPAFFSFGLSSTLQLLAMALECWL 135
Dy 82 TCLISPVVLASYAQNRTLVALGP--ERRVCTYFAFSMTFFSLATMLMLFANALERYLAIG 139
Qy 136 HPFYRRHITLRLGALVAPVVSFAFLAFPCALPFGKFGVQYCGTWCFLQMVHEEGLS 195
Dy 140 HPFYRRHITLRLGALVAPVVSFAFLAFPCALPFGKFGVQYCGTWCFLQMVHEEGLS 195
Qy 196 VLGSYLVLYSSLMALLVATLVLNGLGMRNLYAMHRRILQRHRSCTRDCAEPADGREGASP 255
Dy 196 VLGSYLVLYSSLMALLVATLVLNGLGMRNLYAMHRRILQRHRSCTRDCAEPADGREGASP 255
Dy 196 ---YLRLVATLILLIILAVLACNFSVIVNLHMRGRGRRRCGFSLSGSHRRRAERVSMA- 251
Qy 256 QPLEDHLHLLALLMTLVLCWCSLPVATP 284
Dy 252 ---BETDHLIALLMTITFAVCSLPFTIF 277

RESULT 14
ID P12R BOVIN STANDARD; PRT; 385 AA.
AC P79393;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prostacyclin receptor (prostanoid IP receptor) (PGI receptor)
DE (Prostaglandin 12 receptor).
GN Name=PTGIR;

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hasse A., Schroer K.;
RT "Cloning and sequencing of the bovine prostacyclin receptor gene.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for prostacyclin (prostaglandin 12 or PGI2).
CC The activity of this receptor is mediated by G(s) proteins which
CC activate adenylate cyclase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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or send an email to license@isb-sib.ch).

DR EMBL: Z93039; CAB07510.1; -.
DR EMBL: Z93040; CAB07510.1; JOINED.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR000370; IP_receptor.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR01788; PROSTANOIDR.
DR PRINTS: PR00429; THROMBOXANER.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_3; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Transmembrane.
FT DOMAIN 1 16 Extracellular (Potential).
FT TRANSMEM 17 38 1 (Potential).
FT DOMAIN 39 51 Cytoplasmic (Potential).
FT TRANSMEM 52 76 2 (Potential).
FT DOMAIN 77 94 Extracellular (Potential).
FT TRANSMEM 95 115 3 (Potential).
FT DOMAIN 116 134 Cytoplasmic (Potential).
FT TRANSMEM 135 158 4 (Potential).
FT DOMAIN 159 181 Extracellular (Potential).
FT TRANSMEM 182 208 5 (Potential).
FT DOMAIN 209 234 Cytoplasmic (Potential).
FT TRANSMEM 235 259 6 (Potential).
FT DOMAIN 260 273 Extracellular (Potential).
FT TRANSMEM 274 294 7 (Potential).
FT DOMAIN 295 385 Cytoplasmic (Potential).
FT DISULFID 5 165 By similarity.
FT DISULFID 92 170 By similarity.
FT LIPID 308 308 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 7 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 385 AA; 41247 MW; OGDASA4D18E035C7 CRC64;

Query Match 35.6%; Score 549; DB 1; Length 385;
Best Local Similarity 46.1%; Pred. No. 7.5e-35;
Matches 131; Conservative 36; Mismatches 85; Indels 32; Gaps 8;

Qy 8 QNNTTSVEKNSAVMGVLFSTGLGNLLALGLARSLGWCRRRLPLPSPVYMLVCG 67
Dy 5 CRNLTYVRDSVGPATSTLMFVAGVVGNGLALGLG-----ARRHR--PSAFVLVTG 55
Qy 68 LTVTDLGLKCLSPVVLAAAYQNRSLRVLA---PALDNLSCQAFPAFFSFGLSSTLQLL 124
Dy 56 LGVTDLLGTCLSPVAFVAAVARNSSLGLARGPA----LCDAFAFAMTFFGLASTLILF 111
Qy 125 AMALECWLSLGHFFFYRRHITLRLGALVAPVVSFAFLAFPCALPFGKFGVQYCGTWC 184
Dy 112 AMAVERCALSHPYLVAQLDGPRLRLALPAIYAFCTIFCSLPFLGLGQHQYCPGSGWCF 171
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DR	MGD; MGI:99535; Ptgir.
DR	InterPro; IPR000276; GPCR_Rhodopn.
DR	InterPro; IPR000370; IP_receptor.
DR	InterPro; IPR008365; Prostanoidrecept.
DR	InterPro; IPR001105; Thbox_receptor.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GCRRHODOPSN.
DR	PRINTS; PR01788; PROSTANOIDR.
DR	PRINTS; PR00429; THROMBOXANER.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
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KW	DOMAIN 1
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FT	DOMAIN 66
FT	TRANSMEM 67
FT	DOMAIN 79
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FT	DOMAIN 104
FT	TRANSMEM 105
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FT	TRANSMEM 123
FT	DOMAIN 143
FT	TRANSMEM 144
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FT	5 (Potential).
FT	Cytoplasmic (Potential).
FT	6 (Potential).
FT	Extracellular (Potential).

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GenCore version 5.1.6
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(without alignments)
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Perfect score: 1080

Sequence: 1 atgaagtcgcgcgtctaccg.....acatggatccagctctgtga 1080

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

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2: gb_hlg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1080	100.0	1488	6 AR075987	AR075987 Sequence
2	1080	100.0	1488	6 AR371655	AR371655 Sequence
3	1080	100.0	2970	9 BC040968	BC040968 Homo sapi
4	846	78.3	1216	6 AR270911	AR270911 Sequence
5	846	78.3	1216	9 HSU13132	U31332 Human DP pr
6	846	78.3	156808	2 AC012407	AC012407 Homo sapi
7	846	78.3	187947	2 CNS05TR6	AL365475 Human chr
8	846	78.3	197817	9 CNS05TCS	AL358833 Human chr
9	657	60.8	1315	10 RNU92289	U92289 Rattus nov
10	655.4	60.7	1074	10 AF120101	AF120101 Rattus no
11	655.4	60.7	1240	6 E10040	E10040 Base sequen
12	653.8	60.5	1071	6 E10039	E10039 Base sequen
13	543.8	50.4	895	10 D29764S1	D29764 Mus musculi
14	540.6	50.1	67632	2 AC095991_3	Continuation (4 of
15	540.6	50.1	110000	2 AC112324_0	Continuation (4 of
16	540.6	50.1	110000	2 AC112324_1	Continuation (2 of
17	540.6	50.1	110000	2 AC115635_2	Continuation (3 of
18	540.6	50.1	299134	2 AC128783	AC128783 Rattus no
19	540.6	50.1	349877	2 AC115218	AC115218 Rattus no

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C	24	537.4	49.8	110000	2	AC115635_1	Continuation (2 of
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C	30	359	33.2	232703	2	AC098748	AC098748 Rattus no
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C	32	220.6	20.4	1077	9	AY275471	AY275471 Homo sapi
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C	39	219	20.3	2372	6	AR270878	AR270878 Sequence
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C	44	214.2	19.8	1077	6	AX280935	AX280935 Sequence
C	45	211	19.5	1074	6	AR035825	AR035825 Sequence

ALIGNMENTS

RESULT 1	AR075987	1488 bp	DNA	linear	PAT 30-AUG-2000
LOCUS	AR075987				
DEFINITION	Sequence 4 from patent US 5958723.				
ACCESSION	AR075987				
VERSION	AR075987.1	GI:10002733			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1488)				
TITLE	Abrahamovitz,M., Boile,Y., Metters,K., Sawyer,N. and Slipetz,D.M.				
JOURNAL	DNA encoding prostaglandin receptor DP				
FEATURES	Patent: US 5958723-A 4 28-SEP-1999;				
source	Location/Qualifiers				
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	/mol_type="unasigned DNA"				

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C	10			
C	11			
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C	15			
C	16			
C	17			
C	18			
C	19			

Db 590 CCGGTGTCCTGGCTGCTCAAGCTCAGAACCGAGTCTGCGGTGCTTGGCCCGCATTTG 649

QY 301 GACAACTCGTGTGGCCAAAGCTTGGCTTCTCATGTCCTTTTGGAGCTCTCTGAC 360

Db 650 GACAACTCGTGTGGCCAAAGCTTGGCTTCTCATGTCCTTTTGGAGCTCTCTGAC 709

QY 361 CTGCAACTCTGGGCAATGAGCATGAGATGCTGGCTCTCCCTAGAGGCACTTTTCTTAC 420

Db 710 CTGCAACTCTGGGCAATGAGCATGAGATGCTGGCTCTCCCTAGAGGCACTTTTCTTAC 769

QY 421 CCAAGGCAATCAACCTGGGCTGGGCGGCACTGATGGCCCCGGTGGATGAGCGCTTCTCC 480

Db 770 CCAAGGCAATCAACCTGGGCTGGGCGGCACTGATGGCCCCGGTGGATGAGCGCTTCTCC 829

QY 481 CTGGCTTTCTGCGGCTACCTTTTCAATGAGCTTGGGAAATTCGTGCAATGACTGCCCGG 540

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QY 541 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCTGGGGTACTCT 600

Db 890 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCTGGGGTACTCT 949

QY 601 GTGCTTACTTCCAGCTTATGAGGCTGTGCTGTCTGCTCCCACTGCTGTGCAACTCTCGG 660

Db 950 GTGCTTACTTCCAGCTTATGAGGCTGTGCTGTCTGCTCCCACTGCTGTGCAACTCTCGG 1009

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QY 721 AAGGACTGTGCGGAGCGGCGGCGGAGCGGAGGAAAGCGTCCCTCAGCCCTGAGAGAG 780

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Db 1190 GTAATTTATCGGCTTACTATGAGATTTAAGATGTCAAGAGAAAAACAGACTCT 1249

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RESULT 2

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LOCUS AR371655

DEFINITION Sequence 4 from patent US 6395499.

ACCESSION AR371655

VERSION AR371655.1 GI:34608648

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1488)

AUTHORS Abizmovitz, M., Metters, K., Boie, Y., Sawyer, N. and Slipetz, D.M.

TITLE Methods of identifying modulators of a DP prostaglandin receptor

JOURNAL Patent: US 6395499-A 4 28-MAY-2002;

FEATURES

source 1.1488

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Query Match 100.0%; Score 1080; DB 6; Length 1488;

Best Local Similarity 100.0%; Pred. No. 6.3e-196;

Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACTGCGCTTCTTACCGCTGCGAGAACACCACTCTGTGTGAAAAAGGCAACTGGGCG 60

Db 350 ATGAACTGCGCTTCTTACCGCTGCGAGAACACCACTCTGTGTGAAAAAGGCAACTGGGCG 409

QY 61 GTGATGAGGAGGAGGTGCTCTTCAAGCAACCGGCTCTCTGGGCAACCTGTGGCCGCGGCGT 120

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DEFINITION Homo sapiens prostaglandin D2 receptor (DP), mRNA (cDNA clone
MGC:49004 IMAGE:5769056), complete cds.
ACCESSION BC040968
VERSION BC040968.1 GI:26454885
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2970)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, D., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S.,
Cartegni, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.D.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, D.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schultz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2970)
Strausberg, R.
Direct Submission
Submitted (06-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: anadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://lmln.lnl.gov>
Series: IRAP Plate: 84 Row: m Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
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Best Local Similarity 100.0%; Pred. No. 6; Le-196;
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DB 163 GTGATGGGGGGGTGTCTTTCAGACACCGGCTCTGTGGCAACTGTGGCCCTGGGGCTG 222
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QY 601 GTGCTTACTCAGGCTTATGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
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RESULT 4
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 LOCUS AR270911
 DEFINITION Sequence 1474 from patent US 6500938.
 ACCESSION AR270911
 VERSION AR270911.1 GI:29702145
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1216)
 AUTHORS Au-Young, J. and Seilhamer, J. J.
 TITLE Composition for the detection of signaling pathway gene expression
 JOURNAL Patent: US 6500938-A 1474 31-DEC-2002;
 FEATURES
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 Best Local Similarity 100.0%; Pred. No. 2.8e-151;
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 DB 530 TTCTATACGTGTGTGTGCTGCGCTGACGGGTCACTGCTGTGGGCAAGTGTCTCTAAGC 589
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QY 301 GACAACTCGTGTGTCAGAACCTTTCGCTTCTTATGTCCTTCTTGGGCTCTCTGACA 360
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 VERSION U31332.1 GI:940378
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 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1216)
 AUTHORS Boile, Y., Sawyer, N., Slipetz, D. M., Metters, K. M., and Abramovitz, M.
 TITLE Molecular cloning and characterization of the human prostanoind DP receptor
 JOURNAL J. Biol. Chem. 270 (32), 18910-18916 (1995)

MEDLINE 95370201
 PUBMED 7642548
 REFERENCE 2 (bases 1 to 1216)
 AUTHORS Abramovitz, M. and Boile, Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1995) Mark Abramovitz, Biochemistry and Molecular Biology, Merck Frost Center for Therapeutic Research, P.O. Box 1005, Pointe Claire-Dorval, Quebec H9R 4P8, Canada

FEATURES

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intron

1196. .>1216

Query Match 78.3%; Score 846; DB 9; Length 1216;
Best Local Similarity 100.0%; Pred. No. 2.8e-151;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION
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KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 156808)
Britten, B., Linton, L., Nussbaum, C. and Lander, E.
Homo sapiens chromosome 14, clone RP11-221N7
Unpublished

2 (bases 1 to 156808)
Britten, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Casle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hages, B., Heatford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lenczky, J., Lieu, C., Locke, K., MacDonald, P., Margus, N.,
McEwan, P., McGuirk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tittel, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wymann, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 156808)

REFERENCE
AUTHORS

Britten, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Baetjen, V., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Casle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heatford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lenczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margus, N.,
McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McSheeters, R.,
Meldrum, J., Menues, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivier, T. M., Oliver, J., Peterson, K., Platero, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tittel, A., Travers, M., Triggilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 16, 2000 this sequence version replaced gi:8096911.
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L2358
Center clone name: 221_N_7
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Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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Consensus quality: 142459 bases at least Q40
Consensus quality: 149548 bases at least Q30
Consensus quality: 152199 bases at least Q20
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Insert size: 154308; sum-of-contrigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contrigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

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 1 (bases 1 to 187947)
 Heilig, R., Petit, J.L., Vico, V., Dastiba, C., Robert, C., Mincker, P.,
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Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,
 Gyapay, G., Saurin, W. and Weissbach, J.
 JOURNAL Sequencing of the human chromosome 14
 REFERENCE Unpublished
 AUTHORS 2 (bases 1 to 187947)
 TITLE Genoscope.
 JOURNAL Direct Submission
 Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE. (E-mail : segref@genoscope.cns.fr
 Web : www.genoscope.cns.fr)
 COMMENT Genoscope Center
 Center: Genoscope / Centre National de Sequencage
 Web site: http://www.genoscope.cns.fr/
 Contact: Segref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-262W8 (AC=AL355833)
 Downstream BAC (overlapping the SP6 end) : R-1033H2
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 Assembly program: Phrap; version 2.0
 Quality coverage: 5.57x in Q20 bases; sum-of-contigs

Overall quality chart :
 Range : bases
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 1 - 9 :
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ORIGIN

Query Match 78.3%; Score 846; DB 9; Length 187947;
 Best Local Similarity 100.0%; Pred.No. 2.2e-151;
 Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	103308	GCGATGCGCAACCTCTATGCGATGCAACGCGCGGCTGACAGGCAACCGGCGTCTTGACAC	103249
Qy	721	AGGGACTGTGCCGACCGGCGCGGCAACGGAAGGAAGCGTCTCCCTCAGGCCCTTGAGAGAG	780
Db	103248	AGGGACTGTGCCGACCGGCGCGGCAACGGAAGGAAGCGTCTCCCTCAGGCCCTTGAGAGAG	103189
Qy	781	CTGGATCACCTCTGCTGTGCTGGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGCCC	840
Db	103188	CTGGATCACCTCTGCTGTGCTGGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGCCC	103129
Qy	841	GTAAAT 846	
Db	103128	GTAAAT 103123	

CNS05TCS/c					
LOCUS	CNS05TCS	197817 bp	DNA	linear	PRI 02-MAY-2001
DEFINITION	Human chromosome 14 DNA sequence BAC R-262M8 of library RPcI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.				
ACCESSION	ALJ55833				
VERSION	ALI55833.4	GI:13990340			
KEYWORDS					
SOURCE	HMC				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euarchontomi;				
	Mammalia; Primates; Catarrhini; Hominiidae; Homo.				
	1 (bases 1 to 197817)				
REFERENCE	Hellig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Broctier,P., Caticolico,L., Barde,Y., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruis,T., deBerradinis,V., Cruaud,C., Gyspey,G., Saurin,W. and Weissendbach,J.				
AUTHORS					

TITLE	Sequencing of the human chromosome 14
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 197817)
AUTHORS	Genoscope..
TITLE	Direct Submission
JOURNAL	Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :

COMMENT

Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 197817)
Genoscope.
Direct Submission
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
On May 7, 2001 this sequence version replaced gi:13897294.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contract: Segre@genoscope.cns.fr

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The following BAC sequence is oriented from the T7 to the SP6 end
Upstream BAC (overlapping the T7 end) : R-452D12
Downstream BAC (overlapping the SP6 end) : R-93311 (AC=AL157971)
----- Summary Statistics -----
Assembly program: Phrap, Version 2.0
Quality coverage: 8.90x in Q20 bases; sum-of-contigs

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Overall quality chart

Range	:	Bases
0	:	2
1 - 9	:	4
10 - 19	:	41
20 - 29	:	112
30 - 39	:	876
40 - 49	:	4041
50 - 59	:	8035
60 - 69	:	5759
70 - 79	:	10473
80 - 89	:	37260
90 - 99	:	131214

Percentage of bases with a quality value ≥ 40 : 99 %

FEATURES

1. 19781

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STS

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dbSTS:STS23645
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STS

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identified using the e-PCR software (G. Schuler)"
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STS

ORIGIN

Query Match	78.3%	Score 846	DB 9	Length 197817
Best Local Similarity	100.0%	Pred. No. 2.2e-151		
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Db 160510 ATGAATCGCCGTTTCTACCGCGTCGCCAAGAACACCACTCTGTGGAAAAAGGCAATCTGGCG 160451

QY 61 GGTATGGGGGGGGATGCTTTTCAGAACCGGCGCTCTGGGCAACCTGCTGGCCCTTGGGGCTG 120


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Db 160450 GTGATGCGCGGGGTCCTTTCAGACCGGCTCTGCGGCAACTGTGCTGCGGCTG 160391
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Db 160390 CTGCGCGGCTCGGGGCTGGGGTGTGCTCGCGGCTGCTGCTGCGGCTGCGGCTGCTG 160331
Qy 181 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 160330 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160271
Qy 241 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 160270 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160211
Qy 301 GACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 160210 GACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160151
Qy 361 CTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 160150 CTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160091
Qy 421 CGACGCGCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 160090 CGACGCGCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160031
Qy 481 CTGCGCTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 160030 CTGCGCTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159971
Qy 541 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 159970 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159911
Qy 601 GTGCTCTACTCCAGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 159910 GTGCTCTACTCCAGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159851
Qy 661 GGCATGCGCACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 159850 GGCATGCGCACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 159791
Qy 721 AGGGACTGTCGCGAGCGCGCGCGCGAGAGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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Qy 781 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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Qy 841 GTTATT 846
Db 159670 GTTATT 159665

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RESULT 9
RNU92289 1315 bp mRNA linear ROD 08-MAR-1999
LOCUS RNU92289 1315 bp mRNA linear ROD 08-MAR-1999
DEFINITION Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.
ACCESSION U92289
VERSION U92289.1 GI:2459674
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1315)
Gerahtchenko, D., Beuckmann, C.T., Kanaoka, Y., Eguchi, N.,
Gordon, W.C., Urade, Y., Bazan, N.G. and Hayashi, O.
Dominant expression of rat prostaglandin D2 receptor mRNA in
leptomeninges, inner segments of photoreceptor cells, iris
epithelium, and ciliary processes

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JOURNAL J. Neurochem. 71 (3), 937-945 (1998)
MEDLINE 98387174
PUBMED 9721719
REFERENCE 2 (bases 1 to 1315)
AUTHORS Gerahtchenko, D., Kanaoka, Y., Beuckmann, C. and Urade, Y.
TITLE Direct Submersion
JOURNAL Submitted (07-MAR-1997) Molecular Behavioral Biology, Osaka
Bioscience Institute, 6-2-4 Fureuedai, Suita, Osaka 565, Japan
FEATURES
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ORIGIN

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Query Match 60.8%; Score 657; DB 10; Length 1315;
Best Local Similarity 77.2%; Pred. No. 3, 2e-115;
Matches 830; Conservative 0; Mismatches 230; Indels 15; Gaps 2;

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Qy 72 GGTGCTTTCAGACAGGCTCTGAGCAACCTGCTGAGGCTGAGGCTGAGGCTG 131
Db 129 TGTGCTTTCAGACAGGCTCTGAGCAACCTGCTGAGGCTGAGGCTGAGGCTG 188
Qy 132 GGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 191
Db 189 CGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 248
Qy 192 GGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 251
Db 249 AGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 308
Qy 252 GGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 311
Db 309 GGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 368
Qy 312 GTGCAAGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTC 371
Db 369 ATGTGAAGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTC 428
Qy 372 GGCATGCGCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 431
Db 429 GGCATGCGCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 488
Qy 432 CACCTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 491
Db 489 CACCTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 548
Qy 492 CCGCTACCTTTCATGAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTC 551
Db 549 TCGGCTCCCTTTCATGAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTC 608
Qy 552 TATTCAGATGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
Db 609 CATTCAGATGTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668

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Qy	612	CAGCCTAATGGAGGCGCTGTCGTCTCCGACCGGTGTGAGCAACCTGGCGCATGGCGA	671
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Qy	672	CCTCTATGCGATGCAACCGCGCGCTGCAACCGGCAACCGCGCTCTCTGCAACAGGAACTGTGC	731
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Qy	732	CGAGCCGCGCGCGGAAACGGGAGGAAGCTCCCTTCAGCCCTCTGAGAGAGCTGGATCACTT	791
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Qy	792	CCTGCTGTGCGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGACCGGTAATATATCG	851
Db	849	TGTTCTGTGTGCTCTCAAGACAGTGTCTTACCATGTGTTCCTGCTTTTAATTATCG	908
Qy	852	CGCTTACTATGAGACATTTAAGATGTCAAGAGAAAAACAGACCTTGAAAGACAGA	911
Db	909	TGCTTACTATGAGAGCTTTAAACTTGT-----GGACAGAGCTGACGAGACTCGGA	959
Qy	912	AGACCTCCGAGACCTTGCATTTCTATCTGTGATTTCAATTGTGAGACCTTGGATTTTAT	971
Db	960	AGACCTCCAGACCTTGTGCTTTTCTGTGTGATTTTTCATGTGAGACCTTGTGATTTTAT	1019
Qy	972	CATTTTCAGATCTCCAGATTTTGGATATTTTTCACAAGATTTTTCATTAGACCTTTAG	1031
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Qy	1032	GTACAGAGCGCGGTGACGACATTC-----ACTAACATGGAATCACTGTGTA	1080
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RESULT 10	AF120101	AF120101	1074 bp	mRNA	linear	ROD 10-AUG-2000
LOCUS	AF120101					
DEFINITION	Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.					
ACCESSION	AF120101					
VERSION	AF120101.1					GI:4567037

SOURCE	
ORGANISM	Rattus norvegicus (Norway rat)
	Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1074)	Wright, D.H., Nantel, F., Metters, K.M. and Ford-Hutchinson, A.W.	A novel biological role for prostaglandin D2 is suggested by

distribution studies of the rat DP prostan
Eur. J. Pharmacol. 377 (1), 101-115 (1999)
99376163

PUBMED	10448933
REFERENCE	2 (bases 1 to 1074)
AUTHORS	Wright, D.H. and Abramovitz, M.

TITLE Direct Submission
JOURNAL Submitted (13-JAN-1999) Biochemistry and Molecular Biology, Merck
Frost Centre for Therapeutic Research, P.O. Box 1005, Pointe

source	Claire - Dorval, Quebec H9R 4P8, Canada
FEATURES	Location/Qualifiers
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ORIGIN

Query Match	60.7%;	Score 655.4;	DB 10;	Length 1074;
Best Local Similarity	77.1%;	Pred. No. 6,6e-115;		
Matches 829;	Conservative 0;	Mismatches 231;	Indels 15;	Gaps 2;

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Db 9 GTCCTATCGCTCTCAGGCGACCCACTGGGTGGACA CGGGGCTCTCTCAGCGCAACAAATGGGTG 68

Db 69 TGTGGCTTTCAATGCGAGACTGCTGGGGCAACCTCTGGGGCTGGTGCCTCTGGCGCGATC 128

0y 132 GGGGCTGGGGTGGCTCGCGCGCTCCATGCGGCGCGCGCTCGCTTCATCATGT 191

Db 129 CGGCTGGGGTCTCTGCGGCGCAGGSCCATGTCATTCGCGCGCGCTTCGCTTTTACGTCT 188

192 GGTCTGTGGCCTGACGGTACCCGCTTCTGGGCAAGTCTCTTAAGCCGGGTGCT 251

Db 189 AGTGTGCGGGCTTGACAGTCAACCACTTGCTGGGCGCAAGTGTCTGATCAGCGCCGAGTGTCTT 248

Qy 252 GGTGCTCTACGCTTCAGAACCGGAGTCTGCGGGTCTTGCGCCCGCATTTGGACAACTCGCTT 311

Dbb
249 GGCTGCATACGGCGAAATCGAGCCTTAAGAACTGCTGCTCCCTCAGGCAACCAATT 308

QY 312 GTGCAGGCTTGGCCTTTCATGTCCTTCTTTGGGCTCTCCGACACTGCAACTCCT 371

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372 GGCCATGGCACTGGAGTGTGCTCTCCCTAGGGACCCCTTCTTCTACCGACGGACAT 431

Db 365 GGCATATGGACCTAGAGTCTGGCTGTCTCTGGACACCCCTTTCTTCTACCAAAAGGACAT 428

OY 432 CACCTTGGCTCTGGGCGCACTGGTGGCCCGGTGTGAAGCGCTTCTTCCCTGGCTTTCTG 491

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429 CACCGCCCGCCGGGAGTGTCTGTGGCACAGTCGCGGGCGCTTCTCTTTTGGCTTTCTG 488

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Db 489 TGGCTCTCCCTTTCCTGCTGGCTTTCGGGAATTCGTGCAGTCTGCCCGGACCTGGTGCTT 548

552 TATCCAGATGTTCCACGAGAGGGCTCGCTGTCCGTCTGGGTACTGTGTCTTACTC 611

Db 549 CATCCAGATGATCCACMAAGCCCTATTCTCGATAATAGGCTTCTGTGTGCTTACAC 608

609 CAGCCTCATGCGCTGCTGCTCTCGCACTGTGGTGTGCAACCTGGAGCCATGTCCA 668

672 CCTTATGCGATGACCCGGCGGCTGCGACAGGAACTGTG 731
669 CCTTATGCGATGACAGGCGGACAGGACCAATCCCGCGCTGCTCCAGGAGACCGCG 728

CGAGCCGCGCGGAGGAGCGTCCCCCCTGAGAGACTGATCACCT 791

Db 729 CCACTCAGGCTCAGACTACAGGACATGGGATCCCAATCCTTTGAGAGAGCTGACCACTT 788

Db 789 TGTTCGTGGCTTCACGACAGGCTCTTCACCATGTTCCCTGCCTTAATTATCG 848

Oy 852 CGCTTACTATGAGACATTTAAGCATGTCTAAGAGAAAAACAGACCTCTGGAAGAAGCAGA 911
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193	AGCCTGACATGGTCCCAATTTCATCGA	194
195	AGCCTGACATGGTCCCAATTTCATCGA	196
197	AGCCTGACATGGTCCCAATTTCATCGA	198
199	AGCCTGACATGGTCCCAATTTCATCGA	200

Db 900 AGACCTCCAGGCGTTGCGTTTCGTCGTGATTCATCGTGACCCCTGGATCTTCAT 959

Qy	972	CATTTCAGACTCCAGATATTTGGATATTTTTCACAAGATTTTCATTACACCTTGA	1037
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Qy	1032	GTACAGAGCCGGTCAGACATTC-----ACTAATGGAATCCAGCTGTGA	1080
Db	1020	CTACGAATACTGTGCAGCATTTCTTGGCAGACTAATCATGGAATCCATTGTGA	1074
RESULT 11			
LOCUS	E10040	1240 bp	RNA linear
DEFINITION	Base sequence of DNA including the cDNA encoding prostaglandin D receptor.		
ACCESSION	E10040		
VERSION	E10040.1	GI:22026662	
KEYWORDS	JP 1995258295-A/2.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1240)		
TITLE	Ichikawa,A., Nakao,I. and Narumiya,S.		
JOURNAL	PROSTAGLANDIN D RECEPTOR, ITS PRODUCTION, DNA ENCODING THE SAME RECEPTOR, VECTOR COMPRISING THE SAME DNA AND HOST TRANSFORMED WITH THE SAME VECTOR		
COMMENT	Patent: JP 1995258295-A 2 09-OCT-1995; ONO PHARMACEUT CO LTD OS Mus sp. (mouse) PD JP 1995258295-A/2 PN 09-OCT-1995 PF 22-MAR-1994 JP 1994075382 PI ICHIKAWA ATSUSHI, NAKAO ICHIKAZU, NARUMIYA SHU PC C07K14/705,C12N5/10,C12N15/09,C12P21/02//A61K38/00,(C12P21/02, PC C12R1:91); CC strandedness: Single; CC topology: linear; FH Key Location/Qualifiers FH FT source 1..1240 FT /organism="Mus sp." FT /molecule="genomic RNA" FT CDS 37..1110 FT /product="Prostaglandin D receptor". FT location/Qualifiers 1..1240 /organism="Mus sp." /molecule="genomic RNA" /db_xref="taxon:10095"		
FEATURES	source		
ORIGIN	Query Match 60.7%; Score 655.4; DB 6; Length 1240; Best Local Similarity 77.1%; Fred. No. 6.6e-115; Matches 829; Conservative 0; Mismatches 231; Indels 15; Gaps 2;		
Qy	12	GTTCACCGCTGCAGAACCACTCTGTGGAAAAAGCAACTGGCGGTATGGGCGG	71
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Qy	72	GGTCTCTTCAGACCGGCTCTCTGGGCAACTCTGTGSCCTCTGGGGCTGTGGCGGCTC	131
Db	105	TGTCTCTCTTCGATGTGGGGCTTCTGGGCAATCTTCTGGCGGTGGTGTGGCGGCTC	164
Qy	132	GGGGCTGGGGGTGGTCTGGCGGCTGCACCTGCGCGCGCTCGCTCTTACATGCT	191
Db	165	GGAGATGGGGTCTTTCGCGGCAAGGCGCACTAACCGCGCGCTGTATGTCT	224
Qy	192	GGTGTGGGCTGACGATCACGACTTCTGGGCAAGTCTCTTAAGCCCGGTGTGCT	251
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Qy	252	GGCTGCTACGCTAGAAACCGAGTCTGGGGGTCTTGGCCCGCATGGAACAACCTGTT	311

Db	285	GGCGTCTAAGCGGAAACCAAGACCTTAAGAAAGAACTGCTGCTGCTCTCAGGCAATCAAGT	344
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Db	345	ATGGAAACGCTGCGCTTCCGATGATGTCCTTCTTTGGGCTAGCTCGACCTTAACAGCTGT	404
Qy	372	GGCGATGCGACTGGAAGTGTGCTGCTCTCCCTTAAGGACACCTTTCTTTCAACGAGCAAT	431
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Qy	432	CACCCCTGCGCTGGGCGCACTGATGGGCGCGGATGGTAGCGCTTCTTCCCTGGCTTTCTG	491
Db	465	CACCTTGGCGCGGGAAGTGTGTGGAGACCGGTGTGAGCCGCTTCTGTGCTTTCTG	524
Qy	492	CGCGCTACCTTTCATGAGGCTTTCGGAAATTCGACAGTACTGCCCGGACCTGTGCTT	551
Db	525	TGGGCTCCCTTGGCTGCTGTTTGGGAAGTTCGTGACAGTACTGTCAGGACCTGATGTT	584
Qy	552	TATCAAGATGCTCCAGAGAGAGGCTGCTGTGCTGTGCTGGGATCTGTGTCTTCTACTC	611
Db	585	CATCCAGATATATCCACAGAGAGCGTTTATTTTCGTAATAGGCTTCTCTGTGCTTCTACTC	644
Qy	612	CAGCCTCATGAGCGCTGTGCTGTGCTCTCGCACCGTGTGTCGCAACTCGAGCGCATGCGCA	671
Db	645	CAGCCTCATGAGCGCTGTGCTGTGCTCTCGCACCGTGTGTCGCAACTCGAGCGCATGTCACA	704
Qy	672	CCTCTATGCGATGACACCGGCGGCTGACAGCGGACACCGCGCTCTGCAACAGGACTGTGC	731
Db	705	CCTCTATGAGCATGACAGGCGGCCATAGGACATATCTCACCGCTGTCTCAGGAGACCGGC	764
Qy	732	CGAGCGCGCGCGGACGGAAGGGAAGGCTGCTCCCTCAGCCCTTGAGAGAGCTGATCACT	791
Db	765	CGAGTCAGGCTCAGACTACACAGGAGCGGAGTCCCTGCACTCTTTGGAGAGAGCTGACCACTT	824
Qy	792	CTGCTGCTGCGGCGCTGATGACCGGCTCTTCACTATGATGTTCTGTGCGCGGATTTATTCG	851
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Qy	852	CGCTTACTATGAGACATTTAAGATGTCAAGAGAAAGAAACGAGACTCTGTAAGAGACGA	911
Db	885	TGCGTACTATGAGACCTTTAACTG-----AAGACAAAGCTAAGAGACTGACA	935
Qy	912	AGACCTTCGAGACCTTGGGATTTCTATCTGTGATTTCAATTGTGAGACCTTGGATTTTAT	971
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Qy	1032	GTACAGAGAGCGGTCGAGCAATTC-----ACTAATGAGATTCAGATCTGTGA	1080
Db	1056	CTACAGAAACTGAGAGAGCCATTCCTCCAGCAAAAGTAAGTGAATCCACTTTGTGA	1110

RESULT 12

E10039

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

E10039

Base sequence of the open leading frame of prostaglandin D receptor.

E10039.1

GI:22026661

JP 1995258295-A/1.

unidentified

unclassified

unclassified

1 (bases 1 to 1071)

Ichikawa,A., Nakao,I. and Narumiya,S.

PROSTAGLANDIN D RECEPTOR, ITS PRODUCTION, DNA ENCODING THE SAME RECEPTOR, VECTOR COMPRISING THE SAME DNA AND HOST TRANSFORMED WITH THE SAME VECTOR

Patent: JP 1995258295-A 1 09-OCT-1995;

COMMENT ONO PHARMACEUT CO LTD
 OS Mus.sp (mouse)
 PN JP 1995258295-A/1
 PD 09-OCT-1995
 PF 22-MAR-1994 JP 1994075382
 PT ICHIKAWA ATSUSHI, NAKAO ICHIKAZU, NARUMIYA SHU PC
 C07K14/705, C12N15/10, C12P21/02//A61K38/00, C12P21/02, PC
 C12R1(91);
 CC strandedness: Single;
 CC topology: Linear;
 FH key Location/Qualifiers
 FT source 1..1071
 FT /organism="Mus sp."
 FT /tissue_type="Lung".
 FT Location/Qualifiers
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 /db_xref="taxon:32644"

ORIGIN

Query Match 60.5%; Score 653.8; DB 6; Length 1071;
 Best Local Similarity 77.4%; Pred. No. 1,3e-114;
 Matches 809; Conservative 0; Mismatches 227; Indels 9; Gaps 1;

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 72 GGTGCTCTTACAGACCGGCTCTCTGGGCAACTGTGGCCCTGGGCGCTGCGCGCTC 131
 69 TGTGCTCTTGGGCGGCTCTCTGGGCAACTGTGGCGCTGCTGCTGCGCGCTC 128
 132 GGGGCTGGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 131
 129 GGGAGCTGGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 188
 192 GGTGCTGGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 251
 189 CGTGTGCTGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 248
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 309 ATGCGAAAGCTTGGCTTCTTCAATGCTCTTGGGCTCTCTGCACTGCACTGCTCT 368
 372 GGTGCTGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
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 432 CACCTGCGCTGCGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCT 491
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 609 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
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712 CGAGCCGCGCGGAGAGGAGAAAGCTCCCTCAGCCCTGAGAGAGCTGATCACT 791
 729 CAGTGAAGCTCAGATCACTAGAGGAGGAGGCTCCCTGATCTCTTGGAGAGCTGAGCACTT 788
 792 CCTGCTGCTGGGCTGATGACCGTGTCTTCACTATGCTGCTGCTGCTGCTGCTGCTGCT 851
 789 TGTGCTGCTGGGCTGCTGATGACGCTGCTTCACTGATGCTGCTGCTGCTGCTGCTGCTGCT 848
 852 CGCTTACTATGAGCATTTAAGATGCTCAAGAGGAGAAACAGAGACTCTGAGAGACAGA 911
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 1020 CTACAGAACTGAGAGCAATTCC 1044

RESULT 13
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 LOCUS D2976481 895 bp DNA linear ROD 12-OCT-2002
 DEFINITION Mus musculus gene for prostaglandin D receptor, exon 1.
 ACCESSION D29764
 VERSION D29764.1 GI:577718
 KEYWORDS
 SEGMENT
 SOURCE 1 of 2
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 895)
 Hirata.M., Kakizuka.A., Aizawa.M., Ushikubi.F. and Narumiya.S.
 Molecular characterization of a mouse prostaglandin D receptor and
 functional expression of the cloned gene
 Proc. Natl. Acad. Sci. U.S.A. 91 (23), 11192-11196 (1994)
 95062232
 MEDLINE 7972033
 PUBMED 2 (bases 1 to 895)
 REFERENCE Hirata.M.
 TITLES Direct Submission
 JOURNAL Submitted (01-APR-1994) Masakazu Hirata, Faculty of Medicine, Kyoto
 University, Department of Pharmacology; Yoshida-Kono, Sakyo-ku,
 Kyoto, Kyoto 606, Japan (Tel:81-75-753-4392, Fax:81-75-753-4693)

FEATURES
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 exon 1..879
 /product="prostaglandin D receptor"
 /note="CDS is reported in Acc# D29765."

ORIGIN

Query Match 50.4%; Score 543.8; DB 10; Length 895;
 Best Local Similarity 78.2%; Pred. No. 1,3e-93;
 Matches 653; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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 45 GTCTTATCGCTGACAGATCACTGAGTGAAGGAGGCTCTCGGACAGATGGGCGC 104
 72 GGTGCTCTTACAGACCGGCTCTCTGGGCAACTGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 131

```
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Qy      132 GGGGCTGGGGTGGTGTCTCGCGGCTCCACTGCGCGCGCTGCGCTCCGCTCTTACATGCT 191
Db      165 GGGACTGGGGTCTTGGCGCGGCGGCACTACACCGCGCGCTCCGCTCTTATGCT 224
Qy      192 GGTGTGTGCGCTGACGGTCAACCGACTTGTGGGCAAGTGTCTCTTAAGCCGGTGTGCT 251
Db      225 CGTGTGTGCTTACCGGTCAACCGACTTGTGGGCAAGTGTCTCTTAAGCCGGTGTGCT 284
Qy      252 GGTGTGTGCGCTGACGGTCAACCGAGTGTGCGGGTCTTGGCGCGCTTGGACAATCTGCT 311
Db      285 GGTGTGTGCGCTGACGGTCAACCGAGTGTGCGGGTCTTGGCGCGCTTGGACAATCTGCT 344
Qy      312 GTGCGAAGCTTGGCTCTTCAATGTCCTCTTGGGCTCTCCGCACTGGAACCTCT 371
Db      345 ATGCGAAGCTTGGCTCTTCAATGTCCTCTTGGGCTCTCCGCACTTACGAGCTGT 404
Qy      372 GGGCATGGACCTGAGTGTGCTGCTCTCCCTAGGGCACTTCTTCTTACCGAGCAT 431
Db      405 GGTATGGCGGTGGAAGTGTGCTGCTCTGCTGGAACCTCTTCTTACCAAGGACAT 464
Qy      432 CACCTGCGCTGGGCGGCACTGTGTGCGCGGTGTGAGGCGCTTCTCCCTGCTTCTG 491
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Qy      552 TATCCAGATGTCTCAAGAGAGGCTGCTGTGCTGTGCTGGGTACTGTGTCTTACTC 611
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Qy      612 CAGCTCATGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
Db      645 CAGCTCATGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 704
Qy      672 CCTTATGTGATGTCAACGGGCGGTGTGAGCGGCACTCCGCTCTCTGACCAAGGACTGTG 731
Db      705 CCTTATGTGATGTCAACGGGCGGTGTGAGGCACTTCTTCTTCAAGGAGCGGCG 764
Qy      732 CGAGCGCGCGCGGAGCGGAGGGAAGCTTCCCTCAAGCCCTTGAAGAGCTGATCACT 791
Db      765 CAGTGTAGGCTCAAGTCAAGGAGCGGCTCTGTGCACTCTTGTGAAGAGCTGACACTT 824
Qy      792 CCGTGTGTGCGGTGATGACCGTGTCTTCACTATGTGTCTTCTGCGCGTAATT 846
Db      825 TGTGCTGTGCGCTCTCATGACAGTGTCTTCACTATGTGTCTTCTGCTTAAATT 879
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RESULT 14
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WPCOMMENT
Sequence split into 4 fragments LOCUS AC095991 Accession AC095991

Fragment Name	Begin	End
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AC095991_2	200001	310000
AC095991_3	300001	367632

Continuation (4 of 4) of AC095991 from base 300001 (AC095991 Rattus norvegicus clone CH2)

Query Match 50.1%; Score 540.6; DB 2; Length 67632;

Best Local Similarity 78.0%; Pred. No. 4, 3e-93;

Matches 651; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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Qy      72 GGTGCTCTTACAGACCGGCTCTCTGTGGCAACTGTGCGCTTGGGCTGTGCGCGCTC 131
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Db      63264 CGGGCTGGGGTCTTGGCGCGGCGGCACTGATCCGCGCGCTTGTGTGTGTGTGTGT 63323
Qy      192 GGTGTGTGCGCTGACGGTCAACCGACTTGTGGGCAAGTGTCTCTTAAGCCGGTGTGCT 251
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Db      63504 GGTATGGCACTAAGTGTGCTGCTCTGCTGGAACCTCTTCTTACCAAGGACAT 63563
Qy      432 CACCTGCGCTGGGCGGCACTGTGTGCGCGGTGTGAGGCGCTTCTCCCTGCTTCTG 491
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Qy      492 CGGCTACCTTTTCATGGGCTTGGGGAAGTGTGCGAGTATGCGCCGGGCACTGTGCTT 551
Db      63624 TGGCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 63683
Qy      552 TATCCAGATGTCTCAAGAGAGGCTGCTGTGCTGTGCTGGGTACTGTGTCTTACTC 611
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Db      63744 CAGCTCATGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6803
Qy      672 CCTTATGTGATGTCAACGGGCGGTGTGAGGCGCACTCCGCTCTCTGACCAAGGACTGTG 731
Db      63804 CCTTATGTGATGTCAACGGGCGGTGTGAGGCACTCCGCTCTCTGACCAAGGAGCGGCG 63863
Qy      732 CGAGCGCGCGCGGAGCGGAGGGAAGCTTCCCTCAAGCCCTTGAAGAGCTGATCACT 791
Db      63864 CAGTGTAGGCTCAAGTCAAGGAGCGGCTCTGTGCACTCTTGTGAAGAGCTGACACTT 63923
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RESULT 15
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WPCOMMENT
Sequence split into 4 fragments LOCUS AC112324 Accession AC112324

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AC112324_2	200001	310000
AC112324_3	300001	357027

DEFINITION Rattus norvegicus clone CH230-75L12, *** SEQUENCING IN PROGRESS

ACCESSION AC112324

VERSION AC112324.3 GI:23321735

SOURCE HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

ORGANISM Rattus norvegicus (Norway rat)

REFERENCE 1 (bases 1 to 357027)

AUTHORS Muzny,D.,Marie., Metzker,M.,Lee., Abramzon,S., Adams,C., Alder,J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebich, V., Aoyagi, A., Ayoceli, M., Baca, B., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bismalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Burch, C., Cavazos, I., Caesar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, S., Davy-Carroll, L., De Anda, C., Decker, D., Delgado, O., Dennis, C., Deramo, C., Ding, Y., Dinh, K., Ditya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, L., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Huik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kows, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensunewa, L., Louieged, H., Lozano, R. J., Lu, X., Ma, U., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M. P., McNeill, T. Z., Meenan, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoelameh, O., Okunolu, G., Olapumnsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Pu, M., Quirio, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, R., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X. Z., Sorrelle, R., Soosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanai, K., Valse, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

TITLE

JOURNAL

AUTHORS

JOURNAL

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Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GONG
Center clone name: CH230-75L12

Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 294995 bases at least Q40
Consensus quality: 299994 bases at least Q30
Consensus quality: 302651 bases at least Q20
Estimated insert size: 390689; sum-of-coverage estimation
Quality coverage: 3x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 7987: contig of 7987 bp in length
798 8087: gap of unknown length
808 15583: contig of 7496 bp in length
15584 15683: gap of unknown length
15684 133212: contig of 117529 bp in length
133213 133312: gap of unknown length
133313 261674: contig of 128362 bp in length
261675 261774: gap of unknown length
261775 274519: contig of 12745 bp in length
274520 274619: gap of unknown length
274620 285073: contig of 10454 bp in length
285074 285173: gap of unknown length
285174 327168: contig of 41995 bp in length
327169 327268: gap of unknown length
327269 331337: contig of 4069 bp in length
331338 331437: gap of unknown length
331438 344641: contig of 13204 bp in length
344642 344741: gap of unknown length
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351024 351124: gap of unknown length
351124 357027: contig of 5904 bp in length.

FEATURES

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ORIGIN

Query Match 50.1%; Score 540.6; DB 2; Length 110000;
Best Local Similarity 78.0%; Pred. No. 4.2e-93;
Matches 651; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 12 GTTCTACCGCTGCCAGAACACCCCTCTGTGGAAAAAGGCAACTCGCGGTGATGGCGG 71
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QY 252 GGTGTGTGGCTGTGACAGTCAACGAGTGTGGGGTGTGGCCCGCAATGGGAACTGCT 311
DB 108110 GGTGTGTGGCTGTGACAGTCAACGAGTGTGGGGTGTGGCCCGCAATGGGAACTGCT 108051
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DB 108050 ATGTGAAGCTTGTGCTTCTGATGTCTTCTTGGGTTAGCTCGACTTACGCTACT 107991
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QY 612 CAGCCTCATGGGCTGTGCTGTCTCTGCCACCGTGTGTCAACTGGGCGCATGGCGAA 671
DB 107750 CAGCCTCATGGGCTGTGCTGTCTCTGCCACCGTGTGTCAACTGGGCGCATGGCGAA 107691
QY 672 CCTTATGAGATGCAACGGGCTGTGAGGCGCACCGGCTCTTGCACGAGGACTGTGC 731
DB 107690 CCTTATGAGATGCAACGGGCTGTGAGGCGCACCGGCTCTTGCACGAGGACTGTGC 107631
QY 732 CGAGCCGCGGCGGAGCGGAGGAGAGGCTCCCTCAGCCCTGTGAGAGCTGTATCACT 791
DB 107630 CCAGTCAGGCTCAGACTACAGGATGGGTCCCGAATCTTTGAGAGACTGGACACTT 107571
QY 792 CCTGTGTGTGGGCTGTATACGCTGTCTTCACTATGTGTCTGTGCCGTAATT 846
DB 107570 TGTGTGTGTGGGCTGTATACGCTGTCTTCACTATGTGTCTGTGCCGTAATT 107516

Search completed: April 22, 2005, 15:32:14
Job time : 4919.42 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 09:24:18 ; Search time 652.51 Seconds
(without alignments)
9798.042 Million cell updates/sec

Title: US-10-689-861-3

Perfect score: 1080

Sequence: 1 atgaagtcgcgcttaccg.....acatgaatccagtcgtgtga 1080

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1253	4	ABA09244 Human pro
2	1080	100.0	1253	4	AAs31126 Human pol
3	1080	100.0	1253	10	AD08862 Novel DNA
4	1080	100.0	1303	4	AAs52142 Human pol
5	1080	100.0	1488	2	AAT37402 Prostagla
6	1077	99.7	1077	12	AD030026 Human GPC
7	1051.6	97.4	1264	3	AA27056 Human cel
8	900.4	83.4	1505	10	AD07082 Novel cod
9	846	78.3	1216	3	AAs35105 Human ade
10	846	78.3	1216	3	AA271227 Human low
11	846	78.3	1216	10	AB296921 Human nuc
12	846	78.3	1216	10	ACA56876 Human sig
13	846	78.3	1216	11	ABD20770 Human pul
14	846	78.3	1216	12	AD156672 Human pol
15	846	78.3	14607	3	AA35113 Human ade
16	846	78.3	14607	3	AA271235 Human low
17	846	78.3	14607	3	AB296929 Human nuc
18	846	78.3	14607	11	ABD20778 Human pul
19	829	76.8	964	12	ACH90941 Human gen
20	657	60.8	1074	12	AD030316 Mouse GPC

21	657	60.8	1315	10	AD58427 Toxicity-
22	655.4	60.7	1240	2	AAT05172 Prostagla
23	653.8	60.5	1071	2	AAT05171
24	589	54.5	597	12	ACH76886 Human gen
25	436	40.4	495	3	AA35104 Human ade
26	436	40.4	495	3	AA271226 Human low
27	436	40.4	495	8	AB242748 Human pro
28	436	40.4	495	10	AB296920 Human nuc
29	436	40.4	495	11	ABD20769 Human pul
30	436	40.4	495	13	ADP55148 Human PRO
31	371	34.4	371	12	ACH90586 Human gen
32	220.6	20.4	1077	3	AA34921 Human ade
33	220.6	20.4	1077	3	AA271043 Human low
34	220.6	20.4	1077	10	AB296737 Human pul
35	220.6	20.4	1077	11	ABD20586 Human nuc
36	220.6	20.4	2296	2	AAV12457 Human HP4
37	220.6	20.4	2296	6	ABK88469 Human CDN
38	220.6	20.4	2395	12	AD005737 Human pro
39	220.6	20.4	9060	3	AA34925 Human ade
40	220.6	20.4	9060	3	AA271047 Human low
41	220.6	20.4	9060	10	AB296741 Human pul
42	220.6	20.4	9060	11	ABD20590 Human nuc
43	219	20.3	1077	12	AD030028 Human GPC
44	219	20.3	2372	3	AA34919 Human ade
45	219	20.3	2372	3	AA35106 Human ade

ALIGNMENTS

RESULT 1
ABA09244
ID ABA09244 standard; cDNA; 1253 BP.
XX
AC ABA09244;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human prostaglandin DP receptor homologue cDNA, SEQ ID NO:1020.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytotstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX
OS Homo sapiens.
XX
WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
(HYSE-) HYSEQ INC.
XX
PA Tang YT, Liu C, Drmanac RT;
XX
PI WPI; 2001-457740/49.
XX
DR P-PSDB; ABB12000.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating

or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.

Claim 1; Page 860-861; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides, or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, and thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention

Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;

Query Match 100.0%; Score 1080; DB 4; Length 1253;

Best Local Similarity 100.0%; Pred. No. 1.8e-243; Mismatches 0; Indels 0; Gaps 0; Matches 1080; Conservative 0;

1 ATGAAGTCCCGTCTTACCGCTGCCAGAACACACCTCTGTGAAAAAGGCAACTCGCG 60
122 ATGAAGTCCCGTCTTACCGCTGCCAGAACACACCTCTGTGAAAAAGGCAACTCGCG 181
61 GTGATGGGCGGGTGTCTTTACGACCGCGCTCTTGGGCAACCTGTGGCCCTCGGGGTG 120
182 GTGATGGGCGGGTGTCTTTACGACCGCGCTCTTGGGCAACCTGTGGCCCTCGGGGTG 241
121 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGCGCGTCCACTGCGCCGCTCGGTC 180
242 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGCGCGTCCACTGCGCCGCTCGGTC 301
181 TTCTACATGCTGTGTGTGGCTGACGGTCCACGACTTCTGGGCAAGTGCCTCTCAAGC 240
302 TTCTACATGCTGTGTGTGGCTGACGGTCCACGACTTCTGGGCAAGTGCCTCTCAAGC 361
241 CCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 300
362 CCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 421
301 GACAACTCGTGTGGCAAGCCCTTCTTCATGCTCTCTTGGGCTCTCTCGACA 360
422 GACAACTCGTGTGGCAAGCCCTTCTTCATGCTCTCTTGGGCTCTCTCGACA 481

QY 361 CTGCAACTCTTGGCCATGGCACTGGAGTCTTCCCTAGGACACCTTTCTTCTAC 420
DB 482 CTGCAACTCTTGGCCATGGCACTGGAGTCTTCCCTAGGACACCTTTCTTCTAC 541
QY 421 CGACGGCAATCACCCTCGGCTTGGGCGCACTGGTGGGCGCCCGGTGAGCGCTTCTCC 480
DB 542 CGACGGCAATCACCCTCGGCTTGGGCGCACTGGTGGGCGCCCGGTGAGCGCTTCTCC 601
QY 481 CTGGGCTTTCTGGCGCTACCTTTTCAATGCGTTCGCGGAAGTTCTGTCAGTACTGCCCGC 540
DB 602 CTGGGCTTTCTGGCGCTACCTTTTCAATGCGTTCGCGGAAGTTCTGTCAGTACTGCCCGC 661
QY 541 ACCTGGTCTTTATCCAGATGCTCCACGAGGAGGCTCGCTGTCGGTGTGGGCTTCT 600
DB 662 ACCTGGTCTTTATCCAGATGCTCCACGAGGAGGCTCGCTGTCGGTGTGGGCTTCT 721
QY 601 GTGCTCTACTCAGCTCATGGCGCTGTGCTTCTGCGCACCGTGTGTGCAACTCGC 660
DB 722 GTGCTCTACTCAGCTCATGGCGCTGTGCTTCTGCGCACCGTGTGTGCAACTCGC 781
QY 661 GCATGGCGCAACTCTATGCGATGCAACCGCGGCTGCGAGCGCACCGCGCTCTCGCAC 720
DB 782 GCATGGCGCAACTCTATGCGATGCAACCGCGGCTGCGAGCGCACCGCGCTCTCGCAC 841
QY 721 AGGGAATCTGCGGAGCGCGCGCGAGGAGGAGGCTTCCCTCAGCCCCCTGGAGGAG 780
DB 842 AGGGAATCTGCGGAGCGCGCGCGAGGAGGAGGCTTCCCTCAGCCCCCTGGAGGAG 901
QY 781 CTGATACCTCTCTGCTGCTGCTGATGACCGTCTTCTTCACTATGTGTTCTTCTGCC 840
DB 902 CTGGAATCACTCTCTGCTGCTGCTGATGACCGTCTTCTTCACTATGTGTTCTTCTGCC 961
QY 841 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAGAGGAGAAAAACAGGACCT 900
DB 962 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAGAGGAGAAAAACAGGACCT 1021
QY 901 GAAGAAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGAGACCT 960
DB 1022 GAAGAAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGAGACCT 1081
QY 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTCATT 1020
DB 1082 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTCATT 1141
QY 1021 AGACCTCTTAGGTACAGAGCGGCTGAGCAATTCACATGGAATCCAGTCTGTGA 1080
DB 1142 AGACCTCTTAGGTACAGAGCGGCTGAGCAATTCACATGGAATCCAGTCTGTGA 1201
RESULT 2
AAK53126
ID AAK53126 standard; cDNA; 1253 BP.
XX
AC AAK53126;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2655.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR P-PSDB; AAM79993.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 1; Page 4907; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK51435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1080; DB 4; Length 1253;
 Best Local Similarity 100.0%; Pred. No. 1.8e-243;
 Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAGTCGCGGTTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCAACTCGCGG 60
 DB |||||||
 QY 122 ATGAAGTCGCGGTTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCAACTCGCGG 181
 DB |||||||
 QY 61 GTGATGGCGGGGTGCTCTTACAGACCGGCTCCCTGGGCAACTGCTGGCCCTGGGGCTG 120
 DB |||||||
 QY 182 GTGATGGCGGGGTGCTCTTACAGACCGGCTCCCTGGGCAACTGCTGGCCCTGGGGCTG 241
 DB |||||||
 QY 121 CTGGCGCGCTCGGGGTGGGGGTGGTGTCTCGCGCGGTCCACTGCGCCCGCTGCCCTCGGTC 180
 DB |||||||
 QY 242 CTGGCGCGCTCGGGGTGGGGGTGGTGTCTCGCGCGGTCCACTGCGCCCGCTGCCCTCGGTC 301
 DB |||||||
 QY 181 TTCTACATGCTGGTGTGGCTTGACGGTCAAGCTTCTGGGCAAGTGCCTCTTAAGC 240
 DB |||||||
 QY 302 TTCTACATGCTGGTGTGGCTTGACGGTCAAGCTTCTGGGCAAGTGCCTCTTAAGC 361
 DB |||||||
 QY 241 CCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 300
 DB |||||||
 QY 362 CCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 421
 DB |||||||
 QY 301 GACAACTCGTGTGCCAAGCCTTTCGCTCTTTCATGCTCTTTCGCTCTTTCGCTCTTTCGCTCTTTCG 360
 DB |||||||
 QY 422 GACAACTCGTGTGCCAAGCCTTTCGCTCTTTCATGCTCTTTCGCTCTTTCGCTCTTTCGCTCTTTCG 481
 DB |||||||
 QY 361 CTGCAACTCTTGCGCAATGAGCACTGAGAGTGTGGTCTCTCCCTAGGGCACTCTTCTTCTTCTAC 420
 DB |||||||
 QY 482 CTGCAACTCTTGCGCAATGAGCACTGAGAGTGTGGTCTCTCCCTAGGGCACTCTTCTTCTTCTAC 541
 DB |||||||
 QY 421 CGACGGCACTCACTCTGCGCTTGGGGCGCACTGGTGGCCCGGCTGGTGGCCCTTCTCC 480
 DB |||||||
 QY 542 CGACGGCACTCACTCTGCGCTTGGGGCGCACTGGTGGCCCGGCTGGTGGCCCTTCTCC 601
 DB |||||||

QY 491 CTGGCTTTCTGCGCGCTACCTTTTCATGGGCTTGGGAAGTTTGTGAGTACTGCCCCCGGC 540
 DB |||||||
 QY 602 CTGGCTTTCTGCGCGCTACCTTTTCATGGGCTTGGGAAGTTTGTGAGTACTGCCCCCGGC 661
 DB |||||||
 QY 541 ACCTGGTGTCTTATCCAGATGTCACCGAGGAGGCTCGCTGCGGTGCTGGGTACTCT 600
 DB |||||||
 QY 662 ACCTGGTGTCTTATCCAGATGTCACCGAGGAGGCTCGCTGCGGTGCTGGGTACTCT 721
 DB |||||||
 QY 601 GTGGCTTACTCCAGGCTCATGGCGTGTGTGCTCTCGCCACCGTGTGTGCAACCTCGGC 660
 DB |||||||
 QY 722 GTGGCTTACTCCAGGCTCATGGCGTGTGTGCTCTCGCCACCGTGTGTGCAACCTCGGC 781
 DB |||||||
 QY 661 GCCATGCGCAACTCTATGCGATGACACCGCGGCTGACGGGCAACCGCGCTCTCTGACCC 720
 DB |||||||
 QY 782 GCCATGCGCAACTCTATGCGATGACACCGCGGCTGACGGGCAACCGCGCTCTCTGACCC 841
 DB |||||||
 QY 721 AGGGACTGTGCGGAGCGCGCGGACCGGAGCGGTCCCTCAGCCCTCGAGAGGAG 780
 DB |||||||
 QY 842 AGGGACTGTGCGGAGCGCGCGGACCGGAGCGGTCCCTCAGCCCTCGAGAGGAG 901
 DB |||||||
 QY 781 CTGGATCACCTCTCTGCTGCTGCGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCC 840
 DB |||||||
 QY 902 CTGGATCACCTCTCTGCTGCTGCGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCC 961
 DB |||||||
 QY 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAAAACAGGACCTCT 900
 DB |||||||
 QY 962 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAAAACAGGACCTCT 1021
 DB |||||||
 QY 901 GAAGAGCAGAGACCTCGAGCCTTGGATTTCTCTGATTTCAATTTGAGACCT 960
 DB |||||||
 QY 1022 GAAGAGCAGAGACCTCGAGCCTTGGATTTCTCTGATTTCAATTTGAGACCT 1081
 DB |||||||
 QY 961 TGGATTTTATCATTTTTCAGATCTCAGATTTTCGATATTTTTCACAGATTTTCAAT 1020
 DB |||||||
 QY 1082 TGGATTTTATCATTTTTCAGATCTCAGATTTTCGATATTTTTCACAGATTTTCAAT 1141
 DB |||||||
 QY 1021 AGACCTTTTAGTACAGAGCGGTGACGAATTCATTAACATGAATCCAGTCTGTGA 1080
 DB |||||||
 QY 1142 AGACCTTTTAGTACAGAGCGGTGACGAATTCATTAACATGAATCCAGTCTGTGA 1201
 DB |||||||

RESULT 3
 ADE08862
 ID ADE08862 standard; DNA; 1253 BP.
 XX
 AC ADE08862;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel DNA-related contig nucleotide sequence #106.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; contig; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 22-APR-2002; 2002US-0372615P.
 PR 24-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAK8020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

Seq
 Query Match 100.0%; Score 1080; DB 4; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 1.8e-243; Mismatches 0; Gaps 0;
 Matches 1080; Conservative 0; Indels 0;

Qy 1 ATGAAGTCGCGGCTTCTACCGCTGCCAGAACACACCTCTGTGGAAGGCAACCTCGCGG 60
 Db
 Qy 166 ATGAAGTCGCGGCTTCTACCGCTGCCAGAACACACCTCTGTGGAAGGCAACCTCGCGG 225
 Db
 Qy 61 GTGATGGCGGGGCTCTTTCAGCACCAGCGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 120
 Db 226 GTGATGGCGGGGCTCTTTCAGCACCAGCGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 285
 Qy 121 CTGGCGGCTCGGGGCTGGGGTGGTCTCGGGGCTCCACTGGCGGCGGCTCGGCTCGGTC 180
 Db 286 CTGGCGGCTCGGGGCTGGGGTGGTCTCGGGGCTCCACTGGCGGCGGCTCGGCTCGGTC 345
 Qy 181 TTCTACATGCTGGTGTGGCTGACGCTCACCAGCTTGTGGGCAAGTGTCTCTAAGC 240
 Db 346 TTCTACATGCTGGTGTGGCTGACGCTCACCAGCTTGTGGGCAAGTGTCTCTAAGC 405
 Qy 241 CCGTGTGTGGTGTGGCTGACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCGCAATG 300
 Db 406 CCGTGTGTGGTGTGGCTGACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCGCAATG 465
 Qy 301 GACAACTGTTGTGCAAGCCTTCCGCTTCTCATGCTCTTCTTGGGCTCTCTCGACA 360
 Db 466 GACAACTGTTGTGCAAGCCTTCCGCTTCTCATGCTCTTCTTGGGCTCTCTCGACA 525
 Qy 361 CTGCAACTCTCGGCAATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCTTCTCTAC 420
 Db 526 CTGCAACTCTCGGCAATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCTTCTCTAC 585
 Qy 421 CGACGGCACATCACCTCGGCTGGGCGCACTGTGTGGCCCGCGTGGTGGAGCGCTTCTCC 480
 Db 586 CGACGGCACATCACCTCGGCTGGGCGCACTGTGTGGCCCGCGTGGTGGAGCGCTTCTCC 645
 Qy 481 CTGGCTTCTGGGCGCTACCTTTCATGGGCTTCGGGAAGTGTGTCAGTACTGCCCGCGC 540
 Db 646 CTGGCTTCTGGGCGCTACCTTTCATGGGCTTCGGGAAGTGTGTCAGTACTGCCCGCGC 705
 Qy 541 ACCTGGTCTTTATCCAGATGTCACGAGAGGSGCTCGCTGTGGTGTGGTGTGGTGTGGT 600
 Db 706 ACCTGGTCTTTATCCAGATGTCACGAGAGGSGCTCGCTGTGGTGTGGTGTGGTGTGGT 765
 Qy 601 GTGCTCTACTCAGCGCTCATGGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 660
 Db 766 GTGCTCTACTCAGCGCTCATGGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 825
 Qy 661 GCCATGCGCAACTTATGCGATGACCGCGGCTGTGACGCGCACCCCGCTCTCTGAC 720
 Db 826 GCCATGCGCAACTTATGCGATGACCGCGGCTGTGACGCGCACCCCGCTCTCTGAC 885
 Qy 721 AGGGAATGTCGCGAGCGCGGCGGAGGAGGAGTCCCTCAGCCCTGGAGGAG 780
 Db 886 AGGGAATGTCGCGAGCGCGGCGGAGGAGGAGTCCCTCAGCCCTGGAGGAG 945

Qy 781 CTGGATCACCTCTCTGCTGCTGGCGCTGATGACCGTCTCTTCACTATGTGTCTCTGCCC 840
 Db 946 CTGGATCACCTCTCTGCTGCTGGCGCTGATGACCGTCTCTTCACTATGTGTCTCTGCCC 1005
 Qy 841 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
 Db 1006 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1065
 Qy 901 GAAGAAGCAGAGACCTCTCGAGCCCTTGGGATTTCTATCTGTGATTTCAATTGTGGACCT 960
 Db 1066 GAAGAAGCAGAGACCTCTCGAGCCCTTGGGATTTCTATCTGTGATTTCAATTGTGGACCT 1125
 Qy 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTCCGATATTTTCGATATTTTTCACAAGATTTTCAT 1020
 Db 1126 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCACAAGATTTTCAT 1185
 Qy 1021 AGACCTCTTAGGTACAGGAGCCGTGCAGCAATTCACATACTGAATCCAGTCTGTGA 1080
 Db 1186 AGACCTCTTAGGTACAGGAGCCGTGCAGCAATTCACATACTGAATCCAGTCTGTGA 1245

RESULT 5
 AAT37402
 ID AAT37402 standard; DNA; 1488 BP.
 XX
 AC AAT37402;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Prostaglandin DP receptor coding sequence.
 XX
 KW Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;
 KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
 KW mouse; prostaglandin-related disease; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 349..1429
 FT /*tag= a
 FT /product= "prostaglandin DP receptor"
 XX
 PN WO9623066-A2.
 XX
 PD 01-AUG-1996.
 XX
 PF 23-JAN-1996; 96WO-CA000047.
 XX
 PR 26-JAN-1995; 95US-00378682.
 XX
 PA (MERI) MERCK FROSST CANADA INC.
 XX
 PI Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;
 XX
 XX WPI; 1996-362690/36.
 DR P-PSDB; AAW03516.
 XX
 PT Human prostaglandin DP receptor and related DNA - used to identify
 PT receptor modulators to treat prostaglandin-related diseases.
 XX
 PS Claim 4; Page 41-42; 49pp; English.
 XX
 CC This sequence represents the coding sequence for the human prostaglandin
 CC DP receptor. The DP receptor is the least ubiquitous and least abundant
 CC of the prostanoid receptors. The DP receptors are thought to be
 CC distributed mainly in blood platelets, smooth muscle of various tissues,
 CC and nervous tissue (including the central nervous system). However, many
 CC of the actions and distribution of the DP receptor is species dependent.
 CC The encoded DP receptor is a G protein-coupled receptor which can
 CC specifically bind prostaglandin molecules. This sequence was isolated
 CC using primers (see AAT37403 and AAT37404) based on the N-terminal
 CC sequence, and an internal sequence from purified mouse DP. The human
 CC prostaglandin DP receptor can be used to identify modulators of the

CC receptor. The identified modulators can then be used to treat
CC prostaglandin-related diseases, and for modulating the effects of
CC prostaglandins on the DP receptor

XX SQ Sequence 1488 BP; 232 A; 482 C; 423 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 1080; DB 2; Length 1488;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGAAGTCGCGTCTTACCGCTGCGGAGCAACACCACTCTGTGGAAAAAGGCAACTCGGCG 60
Db 350 ATGAAGTCGCGGTTCTACCGCTGCGGAGCAACCACTCTGTGGAAAAAGGCAACTCGGCG 409
Qy 61 GTGATGCGGCGGTCTCTTCAGACACGCGCTCTCGGCAACCTGCTGCGCCCTGGGGCTG 120
Db 410 GTGATGCGGCGGTCTCTTCAGACACGCGCTCTCGGCAACCTGCTGCGCCCTGGGGCTG 469
Qy 121 CTGGCGCGCTCGGGCTCGGGTGTGTCTCGGGGCTTCCACTGCGCCCGCTGCCCTCGGTC 180
Db 470 CTGGCGCGCTCGGGCTCGGGTGTGTCTCGGGGCTTCCACTGCGCCCGCTGCCCTCGGTC 529
Qy 181 TTCTACATGCTGTGTGTGGCTGACCGGTCAACGACTTGTGGGAAGTGCCTCTTAAGC 240
Db 530 TTCTACATGCTGTGTGTGGCTGACCGGTCAACGACTTGTGGGAAGTGCCTCTTAAGC 589
Qy 241 CCGGTGGTGTGGCTGCTCGCTCAGAACCGAGTCTGCGGGTGTGTCGCGCCGCAATTG 300
Db 590 CCGGTGGTGTGGCTGCTCGCTCAGAACCGAGTCTGCGGGTGTGTCGCGCCGCAATTG 649
Qy 301 GACAACTGCTGTGTGCAAGCCTTCGCTCTTCTATGTCTTCTTTGGGCTCTCTTCGACA 360
Db 650 GACAACTGCTGTGTGCAAGCCTTCGCTCTTCTATGTCTTCTTTGGGCTCTCTTCGACA 709
Qy 361 CTGCAACTCTCGGCATGCGCATGCGAGTGTGCTCTCCCTAGGCGACCTTCTTCTAC 420
Db 710 CTGCAACTCTCGGCATGCGCATGCGAGTGTGCTCTCCCTAGGCGACCTTCTTCTAC 769
Qy 421 CGAGGCAATACCTCGCGCTCGGCGCACTGTGTGGCGCCGCTGTGAGCGCTTCTCC 480
Db 770 CGAGGCAATACCTCGCGCTCGGCGCACTGTGTGGCGCCGCTGTGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTCGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCACTACTGCCCGCG 540
Db 830 CTGGCTTTCTCGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCACTACTGCCCGCG 889
Qy 541 ACCTGGTCTTTATCCAGATGTCACAGAGGCGCTGCTGTGCGTGTGCGGTACTCT 600
Db 890 ACCTGGTCTTTATCCAGATGTCACAGAGGCGCTGCTGTGCGTGTGCGGTACTCT 949
Qy 601 GTGCTCTACTCAGCGCTCATGCGCTGTGCTCTCGCCACCGTGTGCAACTCGGC 660
Db 950 GTGCTCTACTCAGCGCTCATGCGCTGTGCTCTCGCCACCGTGTGCAACTCGGC 1009
Qy 661 GCCATGCGCAACCTCTATGCGATGACCGCGGCTGCGAGCGGCAACCGCGCTCTGCAAC 720
Db 1010 GCCATGCGCAACCTCTATGCGATGACCGCGGCTGCGAGCGGCAACCGCGCTCTGCAAC 1069
Qy 721 AGGACTGTGCGAGCGCGCGGACGAGGAGGAGCGTCCCTCAGCCCTCGAGGAG 780
Db 1070 AGGACTGTGCGAGCGCGCGGACGAGGAGGAGCGTCCCTCAGCCCTCGAGGAG 1129
Qy 781 CTGATACCTCTGCTGCTGCGCTGATGACCGTGTCTTCACTATGTTCTTCGCC 840
Db 1130 CTGATACCTCTGCTGCTGCGCTGATGACCGTGTCTTCACTATGTTCTTCGCC 1189
Qy 841 GTAATTTATCGCGCTTACTATGAGCAATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
Db 1190 GTAATTTATCGCGCTTACTATGAGCAATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1249
Qy 901 GAAAGCAGAGAACCTCCGAGCCTTGGGATTTCTATCTGTGATTTCAATGTGACCT 960
Db 1250 GAAAGCAGAGAACCTCCGAGCCTTGGGATTTCTATCTGTGATTTCAATGTGACCT 1309
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Qy 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTCCGATATTTTTCACAGATTTTCATT 1020
Db 1310 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTCATT 1369
Qy 1021 AGACCTCTTAGGTACAGAGCCGCTGCGCAATTCACACTAATGGAATCCAGTCTGTGA 1080
Db 1370 AGACCTCTTAGGTACAGAGCCGCTGCGCAATTCACACTAATGGAATCCAGTCTGTGA 1429

RESULT 6
ADO30026
ID ADO30026 standard; cDNA; 1077 BP.
XX AC ADO30026;
XX DT 29-JUL-2004 (first entry)
XX Human GPCR PTGDR polynucleotide, SEQ ID NO:1128.
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cystostatic; antinflammatory; vasotropic; antianxiety; antiarrhythmic;
KW CNS; central nervous system; respiratory; antiarrhythmic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX OS Homo sapiens.
XX WO2004040000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
XX P-PSDB; ADO29614.
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 1128; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
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CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 1077 BP; 169 A; 336 C; 310 G; 262 T; 0 U; 0 Other;

Query Match 99.7%; Score 1077; DB 12; Length 1077;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGGTCTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCACTCGGCG 60
DB 1 ATGAAGTCGCGGTCTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCACTCGGCG 60
QY 61 GTGATGGGCGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGTGGCCCTCGGGCTG 120
DB 61 GTGATGGGCGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGTGGCCCTCGGGCTG 120
QY 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGTCCACTGCGCGCTCGCCCTCGGTC 180
DB 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGTCCACTGCGCGCTCGCCCTCGGTC 180
QY 181 TTCTACATCTGTGTGTGCGCTGACGCTCAGGCTTGTGGGCAAGTGCCTCTTAAGC 240
DB 181 TTCTACATCTGTGTGTGCGCTGACGCTCAGGCTTGTGGGCAAGTGCCTCTTAAGC 240
QY 241 CCGGTGGTGTGGCTGCCTACGCTCAGAACCGGAGTCTCGGGTGTCTGCGCCCGCATTTG 300
DB 241 CCGGTGGTGTGGCTGCCTACGCTCAGAACCGGAGTCTCGGGTGTCTGCGCCCGCATTTG 300
QY 301 GACAACTGTTGTGCCAAGCTTTCCTTCAATGCTCTTCTTTGGGCTCTCTCGACA 360
DB 301 GACAACTGTTGTGCCAAGCTTTCCTTCAATGCTCTTCTTTGGGCTCTCTCGACA 360
QY 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGGACCCCTTCTCTAC 420
DB 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGGACCCCTTCTCTAC 420
QY 421 CGACGGCACATCAACCTTGGCGCTGGGCGCACTGGTGGCCCGGCTGTGAGCGCTTCTCC 480
DB 421 CGACGGCACATCAACCTTGGCGCTGGGCGCACTGGTGGCCCGGCTGTGAGCGCTTCTCC 480
QY 481 CTGGCTTTCTGGCGCTTACCTTTTCATGGGCTTGGGAAGTTCGTGAGTACTGCCCCGGC 540
DB 481 CTGGCTTTCTGGCGCTTACCTTTTCATGGGCTTGGGAAGTTCGTGAGTACTGCCCCGGC 540
QY 541 ACCGTGTGCTTTATCCAGATGGTCCACGAGGAGGCTCGCTGCGGTGCTGGGTAATCT 600
DB 541 ACCGTGTGCTTTATCCAGATGGTCCACGAGGAGGCTCGCTGCGGTGCTGGGTAATCT 600
QY 601 GTGCTCTACTCAGCTCTATGGGCTGTGGTCTCTCGCCACCGCTGTGCAACCTCGGC 660
DB 601 GTGCTCTACTCAGCTCTATGGGCTGTGGTCTCTCGCCACCGCTGTGCAACCTCGGC 660
QY 661 GCCATGCGCAACTCTATCGATGCAACCGCGGCTGACGCGGACCCGCGCTCTCGACC 720
DB 661 GCCATGCGCAACTCTATCGATGCAACCGCGGCTGACGCGGACCCGCGCTCTCGACC 720

DB 661 GCCATGCGCAACTCTATCGATGCAACCGCGGCTGACGCGGACCCGCGCTCTCGACC 720
QY 721 AGGGACTGTGCGGAGCGCGCGGAGCGGAGGAGAGCGTCCCTCAGCCCTCTGGAGGAG 780
DB 721 AGGGACTGTGCGGAGCGCGCGGAGCGGAGGAGAGCGTCCCTCAGCCCTCTGGAGGAG 780
QY 781 CTGGATCAGCTCTCTGCTGCTGGCGCTGATGACCGTCTCTTCACTATGTTCTCTGCCC 840
DB 781 CTGGATCAGCTCTCTGCTGCTGGCGCTGATGACCGTCTCTTCACTATGTTCTCTGCCC 840
QY 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAAACAGGACCTCT 900
DB 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAAACAGGACCTCT 900
QY 901 GAAGAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 960
DB 901 GAAGAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 960
QY 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGATTTTCAT 1020
DB 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTTCGGATATTTTTCACAAGATTTTCAT 1020
QY 1021 AGACCTCTTAGGTACAGGAGCGGTCAGCAATTTCCACTAAACATGGAATCCAGTCTG 1077
DB 1021 AGACCTCTTAGGTACAGGAGCGGTCAGCAATTTCCACTAAACATGGAATCCAGTCTG 1077
RESULT 7
AAZ27056
ID AAA27056 standard; cDNA; 1264 BP.
XX
AC AAA27056;
XX AC
DT 22-AUG-2000 (first entry)
XX
DE Human cell surface receptor protein cDNA sequence #13.
XX
KW Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
KW neuroprotective; nontropic; anticonvulsant; cancer; leukaemia; melanoma;
KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 130..1239
FT /*tag= a
FT /product= "HCSR-13"
XX
PN WO20028032-A2.
XX
PD 18-MAY-2000.
XX
PF 12-NOV-1999; 99WO-US026742.
XX
PR 12-NOV-1998; 98US-00191280.
PR 07-DEC-1998; 98US-00206647.
PR 08-MAR-1999; 99US-0123404P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
XX
XX WPI; 2000-376546/32.
DR P-PSDB; AAY94346.
XX
XX New human cell surface receptor protein and polynucleotide useful for
PT diagnosis, prevention and treatment of cancer, immune disorders,
PT infection and neuronal disorders.
XX
PS Claim 9; Page 97; 97pp; English.

XX The present sequence encodes a novel human cell surface receptor protein
CC (HCSR) designated HCSR-13. The nucleotide sequence was identified in
CC Incyte Clone 3576503 from the cDNA library BRONNOT01, which was made from
CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
CC to assemble the consensus sequence. BLAST analysis showed that the
CC sequence is homologous to DR prostanoil receptor g940379. HCSR and its
CC antagonist are useful for preventing or treating disorders associated
CC with decreased or increased expression or activity of HCSR. Such
CC disorders include cancers such as leukaemia and melanoma, immune
CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
CC bacterial and parasitic infections and neuronal disorders such as
CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
CC Polynucleotides encoding HSCRs may be used as hybridisation probes to
CC diagnose these conditions. Anti-HCSR antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing HCSR
CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
CC immunogenic fragments are useful for drug screening using libraries of
CC compounds
XX
SQ Sequence 1264 BP; 189 A; 404 C; 368 G; 303 T; 0 U; 0 Other;

Query Match 97.4%; Score 1051.6; DB 3; Length 1264;
Best Local Similarity 99.4%; Pred. No. 8.4e-237;
Matches 1076; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATGAAGTCGCGGTTTACCGCTGCCGAGACACACACCTCTGTGGAAAAGGCAACTCGCGG 60
DB 130 ATGAAGTCGCGGTTTACCGCTGCCGAGACACACACCTCTGTGGAAAAGGCAACTCGCGG 189

QY 61 GTGATGGCGGGGTGCTTTACAGACCGGCTCTGGGCAACCTGCTGGCCCTGGGGGTG 120
DB 190 GTGATGGCGGGGTGCTTTACAGACCGGCTCTGGGCAACCTGCTGGCCCTGGGGGTG 249

QY 121 CTGGCGCGCTCGGGGTGCGGGTGTGCTCGCGCGTCCACTGCGCGCGCTGCCCTCGGTC 180
DB 250 CTGGCGCGCTCGGGGTGCGGGTGTGCTCGCGCGTCCACTGCGCGCGCTGCCCTCGGTC 309

QY 181 TTCTACATCGTGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
DB 310 TTCTACATCGTGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 369

QY 241 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 370 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429

QY 301 GACAACTCGTGTGCAAGCCTTTCGCTTCTTTCATGCTGCTTTCGCTGCTTTCGCTGCTG 360
DB 430 GACAACTCGTGTGCAAGCCTTTCGCTTCTTTCATGCTGCTTTCGCTGCTTTCGCTGCTG 489

QY 361 CTGCAACTCTGCGCATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 420
DB 490 CTGCAACTCTGCGCATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 549

QY 421 CGAGGCAATACACCTCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 480
DB 550 CGAGGCAATACACCTCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 609

QY 481 CTGGCTTTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 610 CTGGCTTTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669

QY 541 ACTGTGCTTTATTCAGATGTCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 670 ACTGTGCTTTATTCAGATGTCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729

QY 601 GTGCTCTACTCAGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 730 GTGCTCTACTCAGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789

QY 661 GCATCGGCAACCTCTATGCGATGACCGCGGCTGCTGAGCGGCAACCGCGCTCTCTGACC 720
DB 720 GCATCGGCAACCTCTATGCGATGACCGCGGCTGCTGAGCGGCAACCGCGCTCTCTGACC 780

DB 730 GCATCGGCAACCTCTATGCGATGACCGCGGCTGCTGAGCGGCAACCGCGCTCTCTGACC 849

QY 721 AGGACTGTGCGGAGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780

DB 850 AGGACTGTGCGGAGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909

QY 781 CTGGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

DB 910 CTGGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969

QY 841 GTAATTATTCGCGCTTACTATGAGCATTAAAGGATGTCAAGGAGAGAGAGAGAGAGAGAGAG 900

DB 970 GTAATTATTCGCGCTTACTATGAGCATTAAAGGATGTCAAGGAGAGAGAGAGAGAGAGAGAG 1029

QY 901 GAAG 959

DB 1030 GAAG 1089

QY 960 TTGGATTTTATTCATTTTTCAGATCTCCAGATTTTCGGATATTTTTCAGATATTTTTCAGAGA 1018

DB 1090 TTGGATTTTATTCATTTTTCAGATCTCCAGATTTTCGGATATTTTTCAGATATTTTTCAGAGA 1149

QY 1019 TTAGACCTTTTAGGTACAGGAGCGGTCAGCAATTCACATGAGATGAGATGAGATGAGATGAG 1078

DB 1150 TTAGACCTTTTAGGTACAGGAGCGGTCAGCAATTCACATGAGATGAGATGAGATGAGATGAG 1209

QY 1079 GA 1080

DB 1210 GA 1211

RESULT 8
ADE07082
ID ADE07082 standard; DNA; 1505 BP.
XX
AC ADE07082;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel coding sequence (useful for identifying genetic disorders) #148.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder; gene; ds.
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR P-PSDB; ADE07993.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.

useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

Query Match 78.3%; Score 846; DB 3; Length 1216; Best Local Similarity 100.0%; Pred. No. 1.6e-188; Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGTCGCGGTCTTACCGCTGCCAGACACCACTCTGTGAAAAGGCAACTCGCGG 60
350 ATGAAGTCGCGGTCTTACCGCTGCCAGACACCACTCTGTGAAAAGGCAACTCGCGG 409
61 GTGATGGCGGGGTGTCTTACAGACCGCGCTCTGGGCAACTGTGCGCCCTGGGGGTG 120
410 GTGATGGCGGGGTGTCTTACAGACCGCGCTCTGGGCAACTGTGCGCCCTGGGGGTG 469
121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGCTCCACTGCGCGCGCTCGCCCTGGTFC 180
470 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGCTCCACTGCGCGCGCTCGCCCTGGTFC 529
181 TTCTACATGCTGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
530 TTCTACATGCTGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 589
241 CCGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
590 CCGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
301 GACAACTGCTGTGCAAGCTTTCGCTTTCATGCTGCTTTCATGCTGCTTTCATGCTGCTTTC 360
650 GACAACTGCTGTGCAAGCTTTCGCTTTCATGCTGCTTTCATGCTGCTTTCATGCTGCTTTC 709
361 CTGCAACTGCTGCGCATGAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
710 CTGCAACTGCTGCGCATGAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
421 CGAGGCAATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
770 CGAGGCAATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
481 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTGGGAAGTTCTGTCAGTACTGCCCCGGC 540
830 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTGGGAAGTTCTGTCAGTACTGCCCCGGC 889
541 ACCTGCTGCTTTATCCAGATGTCACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
890 ACCTGCTGCTTTATCCAGATGTCACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
601 GTGCTCTACTCCAGCTCATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
950 GTGCTCTACTCCAGCTCATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
661 GCATGCGCAACTCTTATCGATGTCACCGCGGCTGTCAGCGGCAACCGCGCTCTCTGACC 720

1010 GCCATGCGCAACTCTATGCGATGTCACGCGGCTGTCAGCGGCAACCGCGCTCTCTGACC 1069
721 AGGGAGTGTGCGAGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
1070 AGGGAGTGTGCGAGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
781 CTGGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
1130 CTGGATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
841 GPAATT 846
1190 GPAATT 1195

RESULT 10
AAF21227
ID AAF21227 standard; DNA; 1216 BP.
XX
AC AAF21227;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2794.
DE
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cycostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
PT
PT Disclosure; Page 1139; 1592pp; English.
PS
XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cycostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system

CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;
Query Match 78.3%; Score 846; DB 3; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.6e-186;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCGGTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGCGG 60
DB 350 ATGAAGTCGCGGTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGCGG 409
QY 61 GTGATGGGCGGGTGTCTTTACGACACCGCGCTCTCTGGGCAACCTGTGCGCCCTGGGGCTG 120
DB 410 GTGATGGGCGGGTGTCTTTACGACACCGCGCTCTCTGGGCAACCTGTGCGCCCTGGGGCTG 469
QY 121 CTGGGCGCTCGGGGCTGGGGTGGTCTCGCGCGTCCACTGCGCCCGCTGCCCTCGGTC 180
DB 470 CTGGGCGCTCGGGGCTGGGGTGGTCTCGCGCGTCCACTGCGCCCGCTGCCCTCGGTC 529
QY 181 TTCTACATCTGTGTGTGCGCTGACGCTCACCGACTGCTGCGGCAAGTCCCTCAAGC 240
DB 530 TTCTACATCTGTGTGTGCGCTGACGCTCACCGACTGCTGCGGCAAGTCCCTCAAGC 589
QY 241 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTGCGCCCGCATTTG 300
DB 590 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTGCGCCCGCATTTG 649
QY 301 GACAACTGTTGTGCCAAGCTTGGCTTCTCATGTCTCTTTGGGTCTCTCTCGACA 360
DB 650 GACAACTGTTGTGCCAAGCTTGGCTTCTCATGTCTCTTTGGGTCTCTCTCGACA 709
QY 361 CTGCAACTCTGGCCATGCACTGGAGTGTGCTCTCCCTAGGCGACCTTTCTCTAC 420
DB 710 CTGCAACTCTGGCCATGCACTGGAGTGTGCTCTCCCTAGGCGACCTTTCTCTAC 769
QY 421 CGACGGCACATCACCTGCGCCTGGGCGCACTGGTGGCCCGGCTGTGAGCGCTTCTCC 480
DB 770 CGACGGCACATCACCTGCGCCTGGGCGCACTGGTGGCCCGGCTGTGAGCGCTTCTCC 829
QY 481 CTGGCTTTCTGGCGCTACTTTTATGCGCTTCGGGAAGTGTGTCAGTACTGCCCCGGC 540
DB 830 CTGGCTTTCTGGCGCTACTTTTATGCGCTTCGGGAAGTGTGTCAGTACTGCCCCGGC 889
QY 541 ACCTGTGCTTTATCCAGATGTCCACGAGGAGGCTCGCTGCGGTGTGGGTACTCT 600
DB 890 ACCTGTGCTTTATCCAGATGTTCACGAGGAGGCTCGCTGCGGTGTGGGTACTCT 949
QY 601 GTGCTTACTCCAGCTCATGCGGCTGTGCTGCTCCGCCACCGTGTGTGCAACTCTCGCG 660
DB 950 GTGCTTACTCCAGCTCATGCGGCTGTGCTGCTCCGCCACCGTGTGTGCAACTCTCGCG 1009
QY 661 GCATGCGCAACTCTATCGATGACACCGCGGCTGTCAGCGGACCCCGGCTCTCTGACCC 720
DB 1010 GCATGCGCAACTCTATCGATGACACCGCGGCTGTCAGCGGACCCCGGCTCTCTGACCC 1069
QY 721 AGGACTGTGCGGAGCGCGCGGACGAGGAGGCTCTCCCTCAGCCCTGGAGGAG 780
DB 1070 AGGACTGTGCGGAGCGCGCGGACGAGGAGGAGGCTCTCCCTCAGCCCTGGAGGAG 1129

QY 781 CTGGATCACCTCTCTGCTGCTGGCGGTGATGACCGTGCTTTCTACTATGTTCTCTGCC 840
DB 1130 CTGGATCACCTCTCTGCTGCTGGCGGTGATGACCGTGCTTTCTACTATGTTCTCTGCC 1189
QY 841 GTAAAT 846
DB 1190 GTAAAT 1195
RESULT 11
ABZ96921
ID ABZ96921 standard; DNA; 1216 BP.
XX AC ABZ96921;
XX DT 17-OCT-2003 (first entry)
XX Human nucleic acid sequence.
DE Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 12163; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;
SQ

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Query Match      78.3%; Score 846; DB 10; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.6e-188;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGCGG 60
Dd 350 ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGCGG 409
QY 61 GTGATGGCGGGGTGCTCTTACGACACCGGCTCTTGGGCAACCTGCTGGCCCTGGGGCTG 120
Dd 410 GTGATGGCGGGGTGCTCTTACGACACCGGCTCTTGGGCAACCTGCTGGCCCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTGCTCGGGCGCTCCACTGCGCCCGCTGCGCTG 180
Dd 470 CTGGCGCGCTCGGGGCTGGGGTGTGTGCTCGGGCGCTCCACTGCGCCCGCTGCGCTG 529
QY 181 TTCTACATGCTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 240
Dd 530 TTCTACATGCTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 589
QY 241 CCGGTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 300
Dd 590 CCGGTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 649
QY 301 GACAACTGGTGTGCAAGCTTTCGCTTCTTCATGTCTCTTGGGCTCTCTTCGACA 360
Dd 650 GACAACTGGTGTGCAAGCTTTCGCTTCTTCATGTCTCTTGGGCTCTCTTCGACA 709
QY 361 CTGCAACTCTGGCCATGACCTGAGTGTGGCTCTCTCTAGGCAACCTCTTCTTAC 420
Dd 710 CTGCAACTCTGGCCATGACCTGAGTGTGGCTCTCTCTAGGCAACCTCTTCTTAC 769
QY 421 CGACGGCACAATCACTGGCTGTGGCGCACTGTGTGGCGGCGGCTGAGCGCTCTTCC 480
Dd 770 CGACGGCACAATCACTGGCTGTGGCGCACTGTGTGGCGGCGGCTGAGCGCTCTTCC 829
QY 481 CTGGCTTTCTGGCGCTACCTTTTCATGGCTTCGGGAAGTTCGTGCACTGCTGCGCCG 540
Dd 830 CTGGCTTTCTGGCGCTACCTTTTCATGGCTTCGGGAAGTTCGTGCACTGCTGCGCCG 889
QY 541 ACCTGGTGTTCATCCAGATGTCCACGAGGAGGCTCGCTGCGTGTGGGTGCTGCTCT 600
Dd 890 ACCTGGTGTTCATCCAGATGTCCACGAGGAGGCTCGCTGCGTGTGGGTGCTGCTCT 949
QY 601 GTGCTTACTCAGCTCATGGCGCTGTGTGCTTCTGCGCACCGTGTGCAACCTCGCG 560
Dd 950 GTGCTTACTCAGCTCATGGCGCTGTGTGCTTCTGCGCACCGTGTGCAACCTCGCG 1009
QY 661 GCATGCGCAACTCTATGCGATGCAACCGCGGCTGCAAGCGGCTGCTGCGCTGCAAC 720
Dd 1010 GCATGCGCAACTCTATGCGATGCAACCGCGGCTGCAAGCGGCTGCTGCGCTGCAAC 1069
QY 721 AGGGACTGTGCGGAGCGCGCGGAGGAGGAGCGTCTCCCTCAGCCCTGGAGGAG 780
Dd 1070 AGGGACTGTGCGGAGCGCGCGGAGGAGGAGCGTCTCCCTCAGCCCTGGAGGAG 1129
QY 781 CTGGATCACCCTGCTGCTGGCGCTGATGACCGGTGCTCTTCACTATGTGTTCTTGCC 840
Dd 1130 CTGGATCACCCTGCTGCTGGCGCTGATGACCGGTGCTCTTCACTATGTGTTCTTGCC 1189
QY 841 GTAATT 846
Dd 1190 GTAATT 1195

RESULT 12
ID ACAS6876
XX ACAS6876 standard; cDNA; 1216 BP.
AC ACAS6876;
XX ACAS6876;
DT 06-JUN-2003 (first entry)
```

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XX Human signalling pathway polynucleotide probe SEQ ID NO 1474.
DE Human; probe; ss; array element; Parkinson's disease;
XX signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX Homo sapiens.
XX US6500938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX Claim 1; SEQ ID NO 1474; 65pp; English.
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;

Query Match      78.3%; Score 846; DB 10; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.6e-188;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGCGG 60
Dd 350 ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGCGG 409
QY 61 GTGATGGCGGGGTGCTCTTACGACACCGGCTCTTGGGCAACCTGCTGGCCCTGGGGCTG 120
Dd 410 GTGATGGCGGGGTGCTCTTACGACACCGGCTCTTGGGCAACCTGCTGGCCCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTGCTCGGGCGCTCCACTGCGCCCGCTGCGCTG 180
Dd 470 CTGGCGCGCTCGGGGCTGGGGTGTGTGCTCGGGCGCTCCACTGCGCCCGCTGCGCTG 529
QY 181 TTCTACATGCTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 240
Dd 530 TTCTACATGCTGGTGTGGCTGTGCGGTTCACGACTTGTCTGGGCAAGTGCCTCTTAAGC 589
```


Db 830 CTGGCTTTTCGGCGGTACCTTTTCATGGGCTTCGGGAAGTTTCGTGAGTACTGCCCCGGC 889
 QY 541 ACCTGGTGTCTTATCCAGATGTCACAGAGAGGGCTCGCTGTCGGTGTGGGTACTCT 600
 Db 890 ACCTGGTGTCTTATCCAGATGTCACAGAGAGGGCTCGCTGTCGGTGTGGGTACTCT 949
 QY 601 GTGCTTACTCCAGCTTCATGGCGTGTGCTGCTGCGACACCTGCTGTGCAACCTCGGC 660
 Db 950 GTGCTTACTCCAGCTTCATGGCGTGTGCTGCTGCGACACCTGCTGTGCAACCTCGGC 1009
 QY 661 GCCATCGCAACCTCTATCGATGCACCGCGCTGCAGCGGCACCGCGCTCTCGACC 720
 Db 1010 GCCATCGCAACCTCTATCGATGCACCGCGCTGCAGCGGCACCGCGCTCTCGACC 1069
 QY 721 AGGGACTGTCCGAGCGCGCGGACGGAGGGAAGCGTCCCTCAGCCCTCTGGAGGAG 780
 Db 1070 AGGGACTGTCCGAGCGCGCGGACGGAGGGAAGCGTCCCTCAGCCCTCTGGAGGAG 1129
 QY 781 CTGGATCACCTCTGCTGTGGCGCTGATGACCGTGTCTTCACTATGTTCTCTGCC 840
 Db 1130 CTGGATCACCTCTGCTGTGGCGCTGATGACCGTGTCTTCACTATGTTCTCTGCC 1189
 QY 841 GTAATT 846
 Db 1190 GTAATT 1195
 RESULT 15
 ID AAA35113 standard; DNA; 14607 BP.
 AC AAA35113;
 XX
 XX 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2802.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 1064-1068; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;
 Query Match 78.3%; Score 846; DB 3; Length 14607;
 Best Local Similarity 100.0%; Pred. No. 3.6e-188;
 Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAGTCGCGCTTACCGCTGCCAGACACCACTCTGTGAAAAGCACTCGGCG 60
 Db 845 ATGAAGTCGCGCTTACCGCTGCCAGAACACCACTCTGTGAAAAGCACTCGGCG 904
 QY 61 GTGATGGCGGGGTGCTCTTACAGACCGGCTCTCGGGCAACCTGTGCGGCTG 120
 Db 905 GTGATGGCGGGGTGCTCTTACAGACCGGCTCTCGGGCAACCTGTGCGGCTG 964
 QY 121 CTGGCGCGCTCGGGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
 Db 965 CTGGCGCGCTCGGGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1024
 QY 181 TTCTACATGCTGTGTCGGCTGACCGTCACTGGTGGTGGTGGTGGTGGTGGTGGT 240
 Db 1025 TTCTACATGCTGTGTCGGCTGACCGTCACTGGTGGTGGTGGTGGTGGTGGTGGT 1084
 QY 241 CCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
 Db 1085 CCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1144
 QY 301 GACAACTCGTTGTGCCAAGCTTCGCTTTCATGTCTTCTTTGGGTCTCTCTCGACA 360
 Db 1145 GACAACTCGTTGTGCCAAGCTTCGCTTTCATGTCTTCTTTGGGTCTCTCTCGACA 1204
 QY 361 CTGCAACTCTGGCGATGGCACTGGAGTGTGGCTCTCCCTAGGGCACCTCTCTTAC 420
 Db 1205 CTGCAACTCTGGCGCATGGCACTGGAGTGTGGCTCTCCCTAGGGCACCTCTCTTAC 1264
 QY 421 CGACGGCAATCACCTCGCGCTGGCGCACCTGGTGGCGCCCGGTGTGAGCGCTCTCTCC 480
 Db 1265 CGACGGCAATCACCTCGCGCTGGCGCACCTGGTGGCGCCCGGTGTGAGCGCTCTCTCC 1324
 QY 481 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTTGGGAAGTTCGTGAGTACTGCCCCGGC 540
 Db 1325 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTTGGGAAGTTCGTGAGTACTGCCCCGGC 1384
 QY 541 ACCTGGTGTCTTATCCAGATGTCACAGAGAGGGCTCGCTGTCGGTGTGGGTACTCT 600
 Db 1385 ACCTGGTGTCTTATCCAGATGTCACAGAGAGGGCTCGCTGTCGGTGTGGGTACTCT 1444
 QY 601 GTGCTCTACTCCAGCTCATGGCGCTGTGTCCTCGCCACCGTGTGTGCAACCTCGGC 660
 Db 1445 GTGCTCTACTCCAGCTCATGGCGCTGTGTCCTCGCCACCGTGTGTGCAACCTCGGC 1504

Qy	661	GCCATGCGCAACTCTATGCGATGCACCGCGCGCTGCAGCGGCACCCGCGCTCCTGCACC	720
Db	1505	GCCATGCGCAACTCTATGCGATGCACCGCGCGCTGCAGCGGCACCCGCGCTCCTGCACC	1564
Qy	721	AGGGACTGTGCGAGCGCGCGGACGGGAGGGAGGGTCCCTCAGCCCCCTGGAGGAG	780
Db	1565	AGGGACTGTGCGAGCGCGCGGACGGGAGGGAGGGTCCCTCAGCCCCCTGGAGGAG	1624
Qy	781	CTGGATCACCTCCTGCTGCTGGGCTGATGACCGTCTCTTCACTATGTGTCTCTGCC	840
Db	1625	CTGGATCACCTCCTGCTGCTGGGCTGATGACCGTCTCTTCACTATGTGTCTCTGCC	1684
Qy	841	GTAATT	846
Db	1685	GTAATT	1690

Search completed: April 22, 2005, 12:41:21
 Job time : 655.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:55:17 ; Search time 4050.36 Seconds
(without alignments)
10149.570 Million cell updates/sec

Title: US-10-689-861-3
Perfect score: 1080
Sequence: 1 atgaagtcgcccgttaccg.....acatgaatccagtcgtgtga 1080

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	950.6	88.0	1229	6	CD013871	CD013871 90116594
2	655.4	60.7	3190	3	AK032488	AK032488 Mus muscu
3	654	60.6	1053	5	BQ068035	BQ068035 AGENCOURT
C 4	434	40.2	486	1	AI460323	AI460323 ac95401.x
5	393	36.4	495	7	CR747669	CR747669 CR747669
C 6	375.4	34.8	1996	3	AK016503	AK016503 Mus muscu
C 7	361.8	33.5	948	6	BY716183	BY716183 BY716183
8	333	30.8	520	1	AA105532	AA105532 mo57409.r
9	313	29.0	632	2	BB622854	BB622854 BB622854
C 10	311	28.8	589	8	AZ291373	AZ291373 RPI-23-1
11	220.6	20.4	1077	9	AY410679	AY410679 Homo sapi
12	203.4	18.8	1038	3	BC017857	BC017857 Homo sapi
C 13	203.4	18.8	2020	3	CR601077	CR601077 full-length
C 14	202.4	18.7	7565	8	B2120059	B2120059 CH230-523
15	194.8	18.0	2509	3	AK086904	AK086904 Mus muscu
16	192.6	17.8	1032	5	BM925026	BM925026 AGENCOURT
17	192.6	17.8	1077	9	AY410681	AY410681 Mus muscu
18	192.6	17.8	2619	3	AK054132	AK054132 Mus muscu
C 19	186.4	17.3	652	5	BX498371	BX498371 DKFZp779E
C 20	186.2	17.2	658	6	BY724253	BY724253 BY724253
C 21	185.6	17.2	765	1	AU132613	AU132613 AU132613
22	181.2	16.8	615	5	BP381970	BP381970 BP381970
23	180.6	16.7	3079	3	AK036531	AK036531 Mus muscu
24	180.4	16.7	2653	3	AK036474	AK036474 Mus muscu

25	176.4	16.3	571	8	AZ357037	AZ357037 1M0098D23
26	170.6	15.8	1062	5	BM925058	BM925058 AGENCOURT
27	166.2	15.4	635	7	CF131282	CF131282 UI-HF-FQ0
28	162.6	15.1	603	7	CK820125	CK820125 if31906.Y
29	161.8	15.0	1019	1	AL552370	AL552370 AL552370
30	157.4	14.6	646	2	BM629330	BM629330 BM629330
31	154.2	14.3	577	4	BM354213	BM354213 if31906.Y
32	150.2	13.9	562	6	CB609359	CB609359 AMGNNUC:N
33	150.2	13.9	573	4	BM273260	BM273260 if28c08.Y
34	144.2	13.4	655	2	BB625385	BB625385 BB625385
35	139	12.9	771	4	BG919027	BG919027 602816763
36	132	12.2	479	2	AW240093	AW240093 p1r1c.pk0
37	130.4	12.1	264	4	BM338608	BM338608 ha97906.9
38	126.4	11.7	520	1	AA818108	AA818108 UI-R-A0-a
39	123.2	11.4	470	8	AZ278470	AZ278470 RPI-23-1
40	121.6	11.3	653	7	CN484094	CN484094 hw42a07.Y
41	121.2	11.2	584	8	BH341188	BH341188 CH230-51K
42	121.2	11.2	639	8	BH315818	BH315818 CH230-50L
43	121	11.2	733	9	AG414036	AG414036 Mus muscu
44	119.6	11.1	482	5	BM986638	BM986638 EST594232
C 45	118.2	10.9	848	7	CO959749	CO959749 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS CD013871 1229 bp mRNA linear EST 21-OCT-2003
DEFINITION Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION CD013871
VERSION CD013871.1 GI:37777401
KEYWORDS EST:
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1229)
AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Yang, J. and Stuve, L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
JOURNAL Genomics 83 (4), 566-571 (2004)
COMMENT Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES
source Location/Qualifiers
1..1229
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match 88.0%; Score 950.6; DB 6; Length 1229;
Best Local Similarity 91.7%; Pred. No. 2.5e-220;
Matches 1076; Conservative 0; Mismatches 4; Indels 93; Gaps 3;
QY 1 ATGAAGTCGCGCTTACCGTCCAGAACACACCTCTGTGGAAGGCAACCTCGCG 60
Db 4 ATGAAGTCGCGCTTACCGTCCAGAACACACCTCTGTGGAAGGCAACCTCGCG 63
QY 61 GTGATGGCGGGGCTCTTTCAGACCGGCTCTTCGGGCAACCTGTGCGCCCTGGGCTG 120

Db	64	GTGATGGCGGGGTGCTCTTCAGCACCGGCTCTCTCGGGCAACCTGCTGGGCCCTCGGGGCTG	123
Qy	121	CTGCGCGGCTCGGGGCTGGGGTGTGCTCGCGGCTCCATCTGCGCCCGCTGCCCTCGGTC	180
Db	124	CTGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCTCCACTGCGCCCGCTGCCCTCGGTC	183
Qy	181	TTCTACATGCTGTGTGGGCTGACGGTCAACCGACCTGTCTGGGCAAGTGCCTCTAAGC	240
Db	184	TTCTACATGCTGTGTGGGCTGACGGTCAACCGACCTGTCTGGGCAAGTGCCTCTAAGC	243
Qy	241	CCGGTGGTGGTGGCTACGCTCAAGACCGGAGTCTGCGGGTGTGTCGGCCCGGANTG	300
Db	244	CCGGTGGTGGTGGCTACGCTCAAGACCGGAGTCTGCGGGTGTGTCGGCCCGGANTG	303
Qy	301	GACAACTCGTTGTCCAAAGCTTCGCTCTTCAATGTCCTTCTTTGGGCTCTCTCTGACA	360
Db	304	GACAACTCGTTGTCCAAAGCTTCGCTCTTCAATGTCCTTCTTTGGGCTCTCTCTGACA	363
Qy	361	CTGCAACTCTCGGCATGGCACATGGAGTGTGGCTCTCCCTAGGGCACCTCTTCTCTAC	420
Db	364	CTGCAACTCTCGGCATGGCACATGGAGTGTGGCTCTCCCTAGGGCACCTCTTCTCTAC	423
Qy	421	CGACGGCACATCACCTGGGCTGGGGCGACATGGTGGCCCGGTGGTGGAGGCTTCTCC	480
Db	424	CGACGGCACATCACCTGGGCTGGGGCGACATGGTGGCCCGGTGGTGGAGGCTTCTCC	483
Qy	481	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCACTACTGCCCCGGC	540
Db	484	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCACTACTGCCCCGGC	543
Qy	541	ACCTGGTCTTTATCCAGATGGTCCACGAGAGGGCTCGCTGTCTGGTCTGGGGTACTCT	600
Db	544	ACCTGGTCTTTATCCAGATGGTCCACGAGAGGGCTCGCTGTCTGGTCTGGGGTACTCT	603
Qy	601	GTGCTCTACTCCAGCTCATGGCGCTGCTGGTCTCTCGGCACCGTGTCTGTGCACTCTGGC	660
Db	604	GTGCTCTACTCCAGCTCATGGCGCTGCTGGTCTCTCGGCACCGTGTCTGTGCACTCTGGC	663
Qy	661	GCCATGGCAACCTCTATGGATGACCGGGCTGCAGCGGACCGCGCTCTCTGCACTCTGACC	720
Db	664	GCCATGGCAACCTCTATGGATGACCGGGCTGCAGCGGCTGCAGCGGACCGCGCTCTGCACTCTGACC	723
Qy	721	AGGACTGTGCGGACCGCGCGGACGGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	780
Db	724	AGGACTGTGCGGACCGCGCGGACGGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	783
Qy	781	CTGATCACCCTCTGCTGTGGCGCTGATGACCGTGTCTTTCACTATGTGTCTCTGCCC	840
Db	784	CTGATCACCCTCTGCTGTGGCGCTGATGACCGTGTCTTTCACTATGTGTCTCTGCCC	843
Qy	841	GTAATT-----	846
Db	844	GTAATTGATTTGTTCTGGAGTCCCGCCCAAGACACTCGGGAGTAGGTGAGGCTTGAGG	903
Qy	847	-----TATCGCGCTTACTATGGAGCATTT	869
Db	904	AAACATTTTCAGTCTGCTCTCTCTCTTTCTCCCAAGTATCGCGCTTACTATGGAGCATTT	963
Qy	870	TAAGGATGTCAAGGAGAAAAACAGGACCTCTGAAGAAGCAGA-AGACCTCCGAGCCTTGC	928
Db	964	TAAGGATGTCAAGGAGAAAAACAGGACCTCTGAAGAACCAGAGAGACCTCCGAGCCTTGC	1023
Qy	929	GATTTCTATCTGTGATTTCAATTTGGACCTCTGGATTTTATCATTTTTCAGATCTCCAG	988
Db	1024	GATTTCTATCTGTGATTTCAATTTGGACCTCTGGATTTTATCATTTTTCAGATCTCCAG	1083
Qy	989	TATTTCCGATATTTTTTTCACAAGA-TTTTTCATTAGACCTCTTAGGTACAGGAGCCGCTGC	1047
Db	1084	TATTTCCGATATTTTTTTCACAAGATTTTTTCATTAGACCTCTTAGGTACAGGAGCCGATGC	1143
Qy	1048	AGCAATTCCTAAACATGGAAATCCAGTCTGTGA	1080
Db	1144	AGCAATTCCTAAACATGGAAATCCAGTCTGTGA	1176

RESULT 2

AC032488

LOCUS

DEFINITION

AK032488 3190 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643056C09 product:prostaglandin D receptor, full insert sequence.

ACCESSION

AK032488.1 GI:26328308

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, T., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

AUTHORS

Carninci, P., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Taghiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, G., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

TITLE

RISAN Integrated Sequence Analysis System

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

REFERENCE

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
6 bases 1 to 3190
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Numamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saigo, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222).

JOURNAL

Db	842	GCACCCCGAACGTCGGCCAGCC	865
Db	842	GCACCCCGAACGTCGGCCAGCC	865
RESULT 4			
LOCUS	AI460323/c		
DEFINITION	ao95a01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953576 3', similar to SW:PD2R_HUMAN Q13258 PROTAGLANDIN D2 RECEPTOR 1, mRNA sequence.		
ACCESSION	AI460323		
VERSION	AI460323.1	GI:4313204	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 486)		
AUTHORS	Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.		
TITLE	WashU-NCI human EST Project		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyt not found Seq primer: -40UP from Gibco High quality sequence stop: 423.		
FEATURES			
source			
	1..486		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1953576"		
	/sex="female"		
	/tissue_type="meningioma"		
	/dev_stage="72 years"		
	/lab_host="SOLR"		
	/clone_lib="Schiller meningioma"		
	/note="Organ: brain; Vector: pBluescript SK- (Stratagene); Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was prepared from human meningioma using primer 5'-GAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCCGACGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."		
ORIGIN			
Query Match	40.2%;	Score 434;	DB 1; Length 486;
Best Local Similarity	100.0%;	Pred. No. 1.2e-94;	
Matches 434;	Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	647	TGTGCAACTCTGGCGCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGGACC	706
Db	486	TGTGCAACTCTGGCGCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGGACC	427
QY	707	CGCGTCTCTGCACAGGAGCTGTGCGGAGCCGCGCGGAGCGGAGGAGCGTCCCTC	766
Db	426	CGCGTCTCTGCACAGGAGCTGTGCGGAGCCGCGCGGAGCGGAGGAGCGTCCCTC	367
QY	767	AGCCCTCGGAGGAGCTGATACCTCTGCTGGGCTGATGACCTGCTCTTCACTA	826


```

Db      366 AGCCCTCGAGGAGCTGGATCACTCTGCTGCTGGCGGTGATGACCGTGCTCTTCACTA 307
QY      827 TGTGTTCTCTGCCCGTAATTTATTCGCGCTTACTATGAGCAATTAAGGATGTCAAGGAGA 886
Db      306 TGTGTTCTCTGCCCGTAATTTATTCGCGCTTACTATGAGCAATTAAGGATGTCAAGGAGA 247
QY      887 AAAACAGGACCTCTGAAGAGCAGAGACCTCGAGCCTTGCATTTCTATCTGTGATTT 946
Db      246 AAAACAGGACCTCTGAAGAGCAGAGACCTCGAGCCTTGCATTTCTATCTGTGATTT 187
QY      947 CAATTGTGACCTCTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGATATTTTTC 1006
Db      186 CAATTGTGACCTCTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGATATTTTTC 127
QY      1007 ACAAGATTTTCAATAGACCTCTTAGGTACAGGAGCGGTGCAGCAATTCACCTAACATG 1066
Db      126 ACAAGATTTTCAATAGACCTCTTAGGTACAGGAGCGGTGCAGCAATTCACCTAACATG 67
QY      1067 AATCCAGTCTGTGA 1080
Db      66 AATCCAGTCTGTGA 53

RESULT 5
CR747669
LOCUS
DEFINITION
CR747669 495 bp mRNA linear EST 30-AUG-2004
IMAGE:5769056 5', mRNA sequence.
ACCESSION
CR747669
VERSION
CR747669.1 GI:51661368
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 495)
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.,
Peters, M., Radloff, U. and Schneider, D.
I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGP9800912829.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.
Location/Qualifiers
1. .495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP9800912829 ; IMAGE:5769056"
/lab_host="DH10B"
/clone_lib="NIH MGC 121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

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ORIGIN
Query Match 36.4%; Score 393; DB 7; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.1e-84;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAAGTCCCGCTTACCGCTGCCAGAACACCACTCTGTGGAAGGCAACTCGGCG 60
Db      103 ATGAAGTCCCGCTTACCGCTGCCAGAACACCACTCTGTGGAAGGCAACTCGGCG 162
QY      61 GTGATGGGGGGGGTGTCTTTACAGACCGGCTCTTGGGCAACCTGTGCTGCGGGCTG 120
Db      163 GTGATGGGGGGGGTGTCTTTACAGACCGGCTCTTGGGCAACCTGTGCTGCGGGCTG 222
QY      121 CTGGGCGCGCTCGGGGGTGGGGTGGTCTCGCGCGCTCCACTGCGGCGCTCGGTC 180
Db      223 CTGGGCGCGCTCGGGGGTGGGGTGGTCTCGCGCGCTCCACTGCGGCGCTCGGTC 282
QY      181 TTCTACATGCTGTGTGTGGCTTACCGCTCAGAGTACCGGCTTGTGGGCAAGTGCCTTAAGC 240
Db      283 TTCTACATGCTGTGTGTGGCTTACCGCTCAGAGTACCGGCTTGTGGGCAAGTGCCTTAAGC 342
QY      241 CCGGTGGTGTGGCTTACCGCTCAGAGTACCGGCTTGTGGGCAAGTGCCTTGAAGC 300
Db      343 CCGGTGGTGTGGCTTACCGCTCAGAGTACCGGCTTGTGGGCAAGTGCCTTGAAGC 402
QY      301 GACAACTCTTGTGGCAAGCTTCCGCTTCTTCATGTCTCTTTGGGCTCTCTCGACA 360
Db      403 GACAACTCTTGTGGCAAGCTTCCGCTTCTTCATGTCTCTTTGGGCTCTCTCGACA 462
QY      361 CTGCAACTCTTGGCCATGCACTGAGTGTCTGG 393
Db      463 CTGCAACTCTTGGCCATGCACTGAGTGTCTGG 495

RESULT 6
AKO16503/c
LOCUS
DEFINITION
AKO16503 1996 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931433C03 product:unknown EST, full insert
sequence.
ACCESSION
AKO16503
VERSION
AKO16503.1 GI:12855271
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Taghro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

```


ORIGIN

Query Match 29.0%; Score 313; DB 2; Length 632;
Best Local Similarity 76.2%; Pred. No. 3.5e-65;
Matches 385; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 12 GTTCTACCGCTCCAGAACACACCTCTCTGGAAAAGGCAACTCGCGGTGATGGCGG 71
DB 128 GTTCATCTGCTGTCAGACATTCACCTGGGTGGAAAGGGCTCTCTCGGCGACCATGGGCGC 187
QY 72 GGTGCTCTTTCAGCACCGGCTCTCTGGGCAACCTGCTGGGCGCTGCTGGCGGCTC 131
DB 188 TGTGCTCTTTCGGTGGGGCTTCTGGCAATCTTCTGGCGCTGGTCTGCTGGCGGCTC 247
QY 132 GGGGCTGGGGTGGTGTCTCGCGGCTCCACTGCGCGCGCTGCGCCCTCGGTTCTTACATGCT 191
DB 248 GGGACTGGGGTCTTGGCGGCCAGGGCACTACACCGCGCGCTCGGTTCTTTATGTGCT 307
QY 192 GGTGTGGGCTGACGGTCAACGACTTGTGGCAAGTCCCTTAAGCCCGGTGGTGTCT 251
DB 308 CGTGTGGGCTTGGCGGTCAACGACTTGTGGCAATTTGTGATCAGCCCGCATGCTCT 367
QY 252 GGTGCTACGCTCAGAACCGGAGTCTGGGGTGTCTGGCGCGCAATTGGACAACCTCGTT 311
DB 368 GGTGCTACGCGCAACAGAGCTAAGAGACTGCTGCTGCTCAGGCAATCAGTT 427
QY 312 GTGCCAAGCTTTCGCTCTTCTCATGTCCTTTTGGGCTCTCTCGACACTGCAACTCCT 371
DB 428 ATGCGAAGCTTTCGCTCTTCTCATGTCCTTTTGGGCTAGCTCGACCTACAGCTGT 487
QY 372 GGCATGACACTGGAGTGTGCTCTTCTTAGGGCACTCTTCTTCTACCGAGGCAAT 431
DB 488 GGTATGGCGGTGGAGTGTGCTCTTCTGGGCAACCTTCTTCTACCAAAAGCACT 547
QY 432 CACCTGCGCGTGGGCGCACTGTCGCGCGGTGTGGAGCGCTTCTCTCGCTTCTG 491
DB 548 CACCTTGGCGCGGAGTGTGTCGACCGGTGGGCGCGCTTCTGCTTGGCTTTCG 607
QY 492 CGCGTACCTTTCATGGGCTCGGG 516
DB 608 TGCGCTCCCTTGTGGTTTGGG 632

RESULT 10

AZ291373/c
LOCUS
DEFINITION
RPCI-23-131N24, TV RPCI-23 Mus musculus genomic clone
RPCI-23-131N24, genomic survey sequence.

ACCESSION
AZ291373

VERSION
AZ291373.1 GI:9533213

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 589)

Akinret, B., Levens, M., McGann, S., Tsegaye, J., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-131N24.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 131 row: N column: 24
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..589
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-131N24"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 28.8%; Score 311; DB 8; Length 589;
Best Local Similarity 78.8%; Pred. No. 1e-64;
Matches 371; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 376 ATGGCACTGGAGTGTGCTCTCCCTAGGGCACTTCTTCTACGAGGCAATCACC 435
DB 588 ATGGCGGTGAAGTGTGCTCTTGGCAACCTTCTTACCAAGGCACTGTCACC 529
QY 436 CTGCGCTTGGGCGCACTGCTGGCGCGGTGGTGGAGCGCTTCTCCCTGCTTCTGCGG 495
DB 528 TTGCGCGCGGAGTGTGCTGGTGGCACTGCTGGCGCGCTTCTGCTTGTGGG 469
QY 496 CTACCTTTTCATGGGCTTTCGGGAAGTGTGTGAGTACTGCCCCGGCACTGTGTGCTTTATC 555
DB 468 CTCCCTTTTGTGTTTGGGAAGTTCGTGCACTACTGTCCAGGCACTGTGTGTTTCATC 409
QY 556 CAGATGTCACAGAGGAGGCTGCTGCTGGTGTGGGCTACTGTGCTCTACTCCAGC 615
DB 408 CAGATGATCCACAGAGGAGGCTTCTTTCGGTAATAGGCTTCTGTGCTCTACTCCAGC 349
QY 616 CTATGGCGCTGCTGCTCTCGCCACCTGCTGTGCAACCTCGGGCCATGGCAACCTC 675
DB 348 CTATGGCGCTGCTGCTCTCGCAACCTGCTGTGTCACCTGGGTGCCATGTACAACTC 289
QY 676 TATGGGATGACCGCGGCTGAGCGGCACTCGCGCTCTGTGACAGGAGTGTGCGGAG 735
DB 288 TATGACATGACAGCGCGCAGAGGCACTATCTCACCCTGTCTCCAGGAGCGCGCCAG 229
QY 736 CCGCGCGGAGCGGAGGAGGAGCGTCCCTCAGCCCTGGAGGAGCTGATCACCCTCTG 795
DB 228 TCAGGCTCAGACTACAGGCACTGGGTCCTGTCATCTTTGGAGGAGTGTGACCATATG 169
QY 796 CTGCTGGCGCTGATGACCGTCTCTTCTCATATGTTTCTTCTGCCCCGTAATT 846
DB 168 CTGCTGGCTCTCATGACAGTGTCTTTCACCATGTTTCTCCCTGCTTAAATT 118

RESULT 11

AY410679
LOCUS
DEFINITION
Homo sapiens PTGER2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY410679

VERSION
AY410679.1 GI:39766647

KEYWORDS
GSS.

SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AY410679 1077 bp DNA linear GSS 16-DEC-2003

Accession	CR601077.1	GI:50481894
Version	HTC; CNSLT	cdNA.
Keywords	HTC; CNSLT	cdNA.
Source	Human	
Organism	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

REFERENCE	1 (bases 1 to 2020)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue 2 (bases 1 to 2020) Genoscope. Direct Submission
REFERENCE	
AUTHORS	
TITLE	

JOURNAL Direct submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned

FEATURES source 1..2020 Location/Qualifiers
division of Invitrogen.

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t. .2020
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ORIGIN

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Best Local Similarity 61.6%; Pred. No. 2.1e-38;
Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;

Oy 98 GCAACCTGTGGCCCTGCGGCCTCCTCGCGCGTTCGGGGTGTTCTCGCGCGTC 157
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Db 135 GCACCCCTGATGTTCTGTGGCGGTGTGGTGGGCAACGGGGTCTGGCCCCATCTTAGCGC 194

Qy 158 CACTGGCC---CGTGCCCTCGGTCTTACATGCTGGTGTGGGCTGACGGTCACCG 214

Db 195 CAGGGCCACCGGGCGGCCCTCGGCTTCGCGTGTGTGGTACCGACTGGCGGCCACCG 254

[illegible][illegible][illegible]

Accession	Sequence	Position
Db	372 TGACCTCTTTTCGGCGCTCCATGTCATCTCTTTGGCAATGGCCGCTGGCC	431
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Db 432 TGGGGCTGAGCCACCCCTACTCTACGGGCAGCTGGACGGGCCCGCTGGCGCCGGCTGG 491


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QY 455 TGGCCCGCGTGTGAGCGCTTCTCCCTGGCTTCTGGCGCTTACCTTTATGCGGCTCG 514
Db 492 CCGTCCAGCCATCTAGCGCTTCTGGGCTCTCTTCTGGCGCTGCGCTGCGGCTCG 551
QY 515 GGAAGTTCGTGAGTACGCTGCGCGCACCTGTGCTTTATCCAGATGCTCCACGAGGAG 574
Db 552 GCCAACACACAGCACTAGTCCCGCGCGAGCTGTGCTTCTCCCGCATGCGC-----TGGG 605
QY 575 GCTCGCTGCTGCTGCGGCTACTCTGCTCTACTCTACGAGCTCATGGCGCTGCTGCTCC 634
Db 606 CCCAGCGCGCGCGCGCGCTTCTCGCTGCGCTACGCGCGCTGTGTGCGCTGCTGCTGG 665
QY 635 TCGCCACCGCTGCTGCAACCTCGCGCGCATGCGCAACCTCTATGCGATGCAACCGCGCGC 694
Db 666 CTGCGCATCTTCTCTGCAAGGCTCGGTCACTCTGCGCTCTGCGCGCATGATACCGCGC 725
QY 695 TCCAGCGCGCACCGCGCTC 713
Db 726 AGAAGCGCCACCAGGCGTC 744

RESULT 14
BZ120059/c
LOCUS
DEFINITION
CH230-523D17.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-523D17, genomic survey sequence.
ACCESSION
BZ120059
VERSION
BZ120059.1 GI:23761006
KEYWORDS
GSS.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 565)
Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-523D17.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering.information.html). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 523 row: D column: 17
Seq primer: T7
Class: BAC ends.
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/sex="Female"
/cell_type="Brain"
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CHORI-230 Rat (BN/SeNhsd/MCW) BAC library produced by
Pieter de Jong"
ORIGIN
Query Match 18.7%; Score 202.4; DB 8; Length 565;

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Best Local Similarity 68.0%; Pred. No. 2.8e-38;
Matches 336; Conservative 0; Mismatches 136; Indels 22; Gaps 3;
QY 58 GCGGTGATGGCGGGGTGCTCTTACGACACCGCGCTCCCTGGGCAACCTGCTGGCCCTGGGG 117
Db 479 GGGGCAATTTGGGGGTGTGCTCTTTAGTCAGGGGTGCTGACCAACCTTTGGCGGTGGTG 420
QY 118 CTGCTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCGCTCCACATCGCGCGCGCTGCCCTG 177
Db 419 ATGCTGGTGGCTCCAGGCTGGGGTCCCTGCGGCGCAGGGCCACTGACCCACTCCCTAG 360
QY 178 GTCCTTACATGCTGCTGTGCGCTGACGCTGACGCTGACGCTGCTGGGCAAGTGCCTCTTA 237
Db 359 GTATTTTATGTACTAGTGTGTGGCTTGAACGCGCACCAACTTGTCTGGCAAGTGTCTGATC 300
QY 238 AGCCGGTGGTGTGCTGCGCTACGCTCAGAACCGGAGTCTCGGGGTGCTTGGCGCGCA 297
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QY 358 ACCTGCG----AATCTCTGGCAATGGCACTGAGTGTGCTCTCCCTAGGCGACCTTTT 413
Db 179 TCCCTTACTTATGGCTTACTGACTATGCTTGTGAGTGTGCTGCTCTCTCAGACACCCCTT 120
QY 414 CTTCTACCGAGCGGCATCATCCCTGCGCTGCGGCGCTGCGGCGCTGCGGCGCGCTGAGGCG 473
Db 119 CTTCTACCAAAAGGTGCAT---CCTGCGCTGGGAGTGTCTGGTG-----GC 78
QY 474 CTTCTCCCTGGCTTCTGCGGCTTACCTTTTCATGGGCTTGGGAAAGTTCGTGCTGCTG 533
Db 77 TTTCTGTTTAGCTTCTGTCATTCCTTCTGCTGCTTGGGAAAGTTCGTGCTGCTGCTG 18
QY 534 CCGCGCGCACTGGT 547
Db 17 TCCTGGTACTTGGT 4

RESULT 15
AK086904
LOCUS
DEFINITION
Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
library, clone:E030010D19 product:prostaglandin E receptor 2
(subtype EP2), full insert sequence.
ACCESSION
AK086904
VERSION
AK086904.1 GI:26103868
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
AUTHORS
99279253
JOURNAL
MEDLINE
PUBMED
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
20499374
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Ikegami,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,S., Watahiki,M.,

```

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

REFERENCE

6 (bases 1 to 2509)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resesgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>

FEATURES

source
Location/Qualifiers
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ORIGIN

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Best Local Similarity 55.1%; Pred. No. 2.7e-36;
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Qy 119 TGTGTGGCGGCTCGGGGCTGGGGTGGTGTCTCGGGGCTCACTGCGCGCGCTGCC---CT 175
Db 905 TGTGTGGCGGCGGCTGGGGTGGTGTCTCGGGGCTAGCGCGCGGACAGACCTCTATCT 964
Qy 176 CGGTCTTCTACATGCTGGTGTGGGCTGACCGTCAACCGACTTGTCTGGGCAAGTGCCTCC 235
Db 965 CTTTGTTCACCGTGTGGTAAAGGATTTGGTGTCTCACTGACCTGTCTGGGAACCTGCTCA 1024
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Db 1025 TCAGCCGGTGTGTGGTGTGGTGTATTCAGAAACCGAGACCTGTGTGGCGCTGGCTCCCG 1084
Qy 296 CATTGGACAACCTGTGTGGCAAGCTTTCCTCTTCTATGTCTCTTCTTCTTGGGCTCTCCT 355
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Db 1139 CGATGCTCATGCTCTTTCGCTATGGCCTTGAACGCTACCTCTCCATCGGGTACCTTACT 1198
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Db 1199 TCTACAGGCGGCACCTTATCGCGCGCGGGGTCTGGCGGTGTGCTGTCTCATCTATGGGG 1258
Qy 476 TCTCCTGCTGCTTCTGCGGCTACCTTTTCATGGGCTTCGGGAAGTTCGTCAGTACTGCC 535
Db 1259 CCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1318
Qy 536 CCGGCACTGTGTGCTTTTATTCAGATGTTCCACGAGGAGGCTCGCTGTCTGGTGTGGGT 595
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Job time : 4053.36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)

8686.931 Million cell updates/sec

Title: US-10-689-861-3

Perfect score: 1080

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1080	100.0	1488	3	US-09-300-864-4
3	1080	100.0	1488	4	US-09-598-418-4
4	846	78.3	1216	4	US-09-016-434-1474
5	220.6	20.4	2296	1	US-08-239-431A-3
6	220.6	20.4	2296	3	US-09-267-423-3
7	219	20.3	2372	4	US-09-016-434-1441
8	219	20.3	6446	3	US-09-293-170-2
9	214.2	19.8	1077	4	US-09-826-509-558
10	211	19.5	1074	2	US-08-463-081B-29
11	211	19.5	1074	2	US-08-461-379A-29
12	211	19.5	1074	2	US-08-462-390B-29
13	211	19.5	1074	3	US-08-463-074B-29
14	211	19.5	1074	3	US-08-465-585C-29
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18	211	19.5	2450	2	US-08-462-190B-5
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24	201.8	18.7	1356	3	US-09-039-798-5
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33	107.2	9.9	1376	4	US-09-016-434-1361	Sequence 1361, Ap
34	107.2	9.9	1394	2	US-08-068-729-3	Sequence 3, Appli
35	107.2	9.9	1394	3	US-09-255-671-3	Sequence 3, Appli
36	107.2	9.9	1394	3	US-09-395-366-3	Sequence 3, Appli
37	101.2	9.4	1467	4	US-09-826-509-560	Sequence 560, App
38	101.2	9.4	1958	1	US-08-115-365-1	Sequence 1, Appli
39	101.2	9.4	1958	1	US-08-586-897-1	Sequence 1, Appli
40	101.2	9.4	1958	4	US-09-016-434-1380	Sequence 1380, Ap
41	99	9.2	2442	1	US-08-390-162-5	Sequence 5, Appli
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44	82.6	7.6	2932	4	US-09-054-272-5	Sequence 5, Appli
45	71.6	6.6	5688	3	US-09-293-170-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-812-203-4
; Sequence 4, Application US/08812203
; Patent No. 5958723
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,203
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-203-4

Query Match 100.0%; Score 1080; DB 2; Length 1488;
Best Local Similarity 100.0%; Pred. No. 8.4e-256;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GTGATGGCGGGGTGCTCTTACGACCGGCTCTCTGGGCAACTGCTGGCCCTGGGGCTG	120
Db	410	GTGATGGCGGGGTGCTCTTACGACCGGCTCTCTGGGCAACTGCTGGCCCTGGGGCTG	469
Qy	121	CTGGCGGCTCGGGGCTGGGTGGTGCTCGCGGCTCACTGCGCCGCTGCCCTCGGTC	180
Db	470	CTGGCGGCTCGGGGCTGGGTGGTGCTCGCGGCTCACTGCGCCGCTGCCCTCGGTC	529
Qy	181	TTCTACATGCTGTGTGTGCGCTGACGGTCAACCGACTTGTGTGGGCAAGTGCCTCCTAAGC	240
Db	530	TTCTACATGCTGTGTGTGCGCTGACGGTCAACCGACTTGTGTGGGCAAGTGCCTCCTAAGC	589
Qy	241	CCGGTGGTGCTGGCTGCTCAAGCTCAGAACCGGAGTCTGCGGGTGTCTTGGCCCGCGATTG	300
Db	590	CCGGTGGTGCTGGCTGCTCAAGCTCAGAACCGGAGTCTTGGGGTGTCTTGGCCCGCATTTG	649
Qy	301	GACAACTCGTTGTGCCAAGCTTTCGCTTCTTCAATGTCCTTCTTGGGCTCTCTCTGACAA	360
Db	650	GACAACTCGTTGTGCCAAGCTTTCGCTTCTTCAATGTCCTTCTTGGGCTCTCTCTGACAA	709
Qy	361	CTGCAACTCTCGCCATGCGCACTGGAGTGTGCTCTCCCTAGGGCAACCTTCTTCTTCTAC	420
Db	710	CTGCAACTCTCGCCATGCGCACTGGAGTGTGCTCTCCCTAGGGCAACCTTCTTCTTCTAC	479
Qy	421	CGACGGCAATCACTCTCGCTGGCGCACTGGTGGCCCCGGTGTGAGCGCTTCTCTCC	480
Db	770	CGACGGCAATCACTCTCGCTGGCGCACTGGTGGCCCCGGTGTGAGCGCTTCTCTCC	539
Qy	481	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTGGGAGTTCGTGCACTACTGCCCGGC	540
Db	830	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTGGGAGTTCGTGCACTACTGCCCGGC	599
Qy	541	ACCTGTGTCTTTATCCAGATGGTCCAGAGAGGGCTCGCTGTGGTGTCTGGGGTACTCT	600
Db	890	ACCTGTGTCTTTATCCAGATGGTCCAGAGAGGGCTCGCTGTGGTGTCTGGGGTACTCT	659
Qy	601	GTGCTCTACTCCAGCTCATGGGCTGTGGTCTCTCGGCAACGGTGTGTGCACTCTGGC	660
Db	950	GTGCTCTACTCCAGCTCATGGGCTGTGGTCTCTCGGCAACGGTGTGTGCACTCTGGC	719
Qy	661	GCCATGGCAACCTCTATGCGATGCACCGCGGCTGCAGCGGACCCCGGCTCTCTGACC	720
Db	1010	GCCATGGCAACCTCTATGCGATGCACCGCGGCTGCAGCGGACCCCGGCTCTCTGACC	779
Qy	721	AGGGACTGTGCCAGCGCGCGGACGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	780
Db	1070	AGGGACTGTGCCAGCGCGCGGACGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	839
Qy	781	CTGGATCACTCTGTCTGTGGGCTGATGACCGTGTCTTCTCACTATGTGTTCTCTGCC	840
Db	1130	CTGGATCACTCTGTCTGTGGGCTGATGACCGTGTCTTCTCACTATGTGTTCTCTGCC	899
Qy	841	GTAATTTATCGCGTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGACCTCT	900
Db	1190	GTAATTTATCGCGTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGACCTCT	959
Qy	901	GAGAAGCAGAACTCTCGAGCGCTTGGATTTCTATCTGTGATTTCAATTGTGGACCT	960
Db	1250	GAGAAGCAGAACTCTCGAGCGCTTGGATTTCTATCTGTGATTTCAATTGTGGACCT	1019
Qy	961	TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGATTTTCAT	1020
Db	1310	TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGATTTTCAT	1079
Qy	1021	AGACCTCTTAGGTACAGGACCGGTGCAGCAATTCACATAACATGGAATCCAGTCTGTGA	1080
Db	1370	AGACCTCTTAGGTACAGGACCGGTGCAGCAATTCACATAACATGGAATCCAGTCTGTGA	1139

RESULT 2
 US-09-300-864-4
 ; Sequence 4, Application US/09300864
 ; Patent No. 6214972
 ; GENERAL INFORMATION:
 ; APPLICANT: ABRAMOVITZ, MARK
 ; APPLICANT: BOIE, YVES
 ; APPLICANT: SAWYER, NICOLE
 ; APPLICANT: METTERS, KATHLEEN
 ; APPLICANT: SLIPETZ, DEBORAH
 ; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: JOHN W. WALLEN, III
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/300.864
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/378,682
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WALLEN III, JOHN W.
 ; REGISTRATION NUMBER: 35,403
 ; REFERENCE/DOCKET NUMBER: MRL 94/185
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)594-3905
 ; TELEX: (908)594-4720
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1488 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-300-864-4

Query Match	100.0.0.%;	Score 1080;	DB 3;	Length 1488;
Best Local Similarity	100.0.0.%;	Pred. No. 8.4e-258;		
Matches 1080;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGAAGTCGGCGTTCTACCGCTGCCAGAACACACACCTCTGTGAAAAGGCAACTCGGCG	60	
Db	350	ATGAAGTCGGCGTTCTACCGCTGCCAGAACACACACCTCTGTGAAAAGGCAACTCGGCG	409	
Qy	61	GTGATGGCGGGGTGCTCTTCAGCACCGGCTCCTCGGGCAACTGCTGGGCCCTGGGGCTG	120	
Db	410	GTGATGGCGGGGTGCTCTTCAGCACCGGCTCCTCGGGCAACTGCTGGGCCCTGGGGCTG	459	
Qy	121	CTGGCGCGCTCGGGGCTGGGGTGGTGCTCGCGCGCTCACTGCGCCCGCTGCCCTCGGTC	180	
Db	470	CTGGCGCGCTCGGGGCTGGGGTGGTGCTCGCGCGCTCACTGCGCCCGCTGCCCTCGGTC	529	
Qy	181	TTCTACATGCTGGTGCTGCGCTGACGGTCACCGACTTGCTGGGCAAGTGCTCTTAAGC	240	
Db	530	TTCTACATGCTGGTGCTGCGCTGACGGTCACCGACTTGCTGGGCAAGTGCTCTTAAGC	589	
Qy	241	CCGGTGGTGCTGGCTGCCTACGCTCAGAACCGGAGTGCTGGGGTGCTTGGCCCGCGCATTG	300	
Db	590	CCGGTGGTGCTGGCTGCCTACGCTCAGAACCGGAGTGCTGGGGTGCTTGGCCCGCGCATTG	649	
Qy	301	GACAACTCGTTGTGCCAAGCCTTCGCGCTCTTTCATGTCTCTTTGGGGCTCTCCTCGACA	360	

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Db 650 GACAACTCGTGTGCGCAAGCTTCGCTCTTCTATGCTCTTCTTGGGCTCTCTCGACA 709
Qy 361 CTGCAACTCTCGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCGAACCTTTCTTCTAC 420
Db 710 CTGCAACTCTCGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCGAACCTTTCTTCTAC 769
Qy 421 CGACGGCACATCACTCTGCGCTTGGGGGCACTGGTGGCCCGGTGGTGGAGCGCTTCTCC 480
Db 770 CGACGGCACATCACTCTGCGCTTGGGGGCACTGGTGGCCCGGTGGTGGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
Db 830 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 889
Qy 541 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGCTACTCT 600
Db 890 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGCTACTCT 949
Qy 601 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCCACCGTGTGTGCAACCTCGGC 660
Db 950 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCCACCGTGTGTGCAACCTCGGC 1009
Qy 661 GCATCGGCACCTCTATCGATGTCACCGCGGCTCGAGGGCACCGGCTCTCTGCACC 720
Db 1010 GCATCGGCACCTCTATCGATGTCACCGCGGCTCGAGGGCACCGGCTCTCTGCACC 1069
Qy 721 AGGAGCTGTGCCAGCGCGCGGAGCGGAGGAGCGTCCCTCAGGCCCTTGGAGGAG 780
Db 1070 AGGAGCTGTGCCAGCGCGCGGAGCGGAGGAGCGTCCCTCAGGCCCTTGGAGGAG 1129
Qy 781 CTGGATCACTCTCTGTGTGGCGCTGATGACCGTGTCTTCACTATGTGTCTTGTGCC 840
Db 1130 CTGGATCACTCTCTGTGTGGCGCTGATGACCGTGTCTTCACTATGTGTCTTGTGCC 1189
Qy 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAACAGGACCTCT 900
Db 1190 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAACAGGACCTCT 1249
Qy 901 GAAGAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTGGAGCCCT 960
Db 1250 GAAGAGCAGAGAACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTGGAGCCCT 1309
Qy 961 TGGATTTTATCATTTTCAGATCTCAGTATTTTCGATATTTTTCACAAGATTTTCATT 1020
Db 1310 TGGATTTTATCATTTTCAGATCTCAGTATTTTCGATATTTTTCACAAGATTTTCATT 1369
Qy 1021 AGACCTTTAGTACAGGAGCGGTGACGCAATTCACCTAAATGCAATCCAGTCTGTGA 1080
Db 1370 AGACCTTTAGTACAGGAGCGGTGACGCAATTCACCTAAATGCAATCCAGTCTGTGA 1429
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RESULT 3

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US-09-598-418-4
; Sequence 4, Application US/09598418
; Patent No. 6395499
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; BOJE, YVES
; SAWYER, NICOLE
; METTERS, KATHLEEN
; SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,418
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-598-418-4
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Query Match 100.0%; Score 1080; DB 3; Length 1488;
Best Local Similarity 100.0%; Pred. No. 8.4e-258;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGTCCGCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 60
Db 350 ATGAAGTCCGCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 409
Qy 61 GTGATGGCGGGGTGCTCTTTCAGCACCGGCTCTCTGGCAACCTGTGCGCCCTGGGGCTG 120
Db 410 GTGATGGCGGGGTGCTCTTTCAGCACCGGCTCTCTGGCAACCTGTGCGCCCTGGGGCTG 469
Qy 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGCTGCACTGGCGCGCTGCGCTCGGTC 180
Db 470 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGCTGCACTGGCGCGCTGCGCTCGGTC 529
Qy 181 TTCTCATGCTGTGTGGCTGACCGGTCAACGACTTCTGGGCAAGTGCCTCTTAAGC 240
Db 530 TTCTCATGCTGTGTGGCTGACCGGTCAACGACTTCTGGGCAAGTGCCTCTTAAGC 589
Qy 241 CGCGTGTGTGGCTGCTTACGCTCAGAACCGGAGTCTCGGGTGTCTGCGCCCGCATG 300
Db 590 CGCGTGTGTGGCTGCTTACGCTCAGAACCGGAGTCTCGGGGTGTCTGCGCCCGCATG 649
Qy 301 GACAACTGTGTGCAAGCCTTCGCTTCTTTCATGTCCTTCTTTGGGCTCTCTCGACA 360
Db 650 GACAACTGTGTGCAAGCCTTCGCTTCTTTCATGTCCTTCTTTGGGCTCTCTCGACA 709
Qy 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCGAACCTTTCTTCTAC 420
Db 710 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCGAACCTTTCTTCTAC 769
Qy 421 CGACGGCACATCACTCTGCGCTTGGGGGCACTGGTGGCCCGGTGGTGGAGCGCTTCTCC 480
Db 770 CGACGGCACATCACTCTGCGCTTGGGGGCACTGGTGGCCCGGTGGTGGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
Db 830 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 889
Qy 541 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGCTACTCT 600
Db 890 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGCTACTCT 949
Qy 601 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCCACCGTGTGTGCAACCTCGGC 660
Db 950 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCCACCGTGTGTGCAACCTCGGC 1009
Qy 661 GCCATGCGCAACCTCTATGCGATGTCACCGCGGCTCGAGGGCACCGGCTCTCTGCACC 720
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Db 1010 GCCATGCGCAACCTCTATGCGATGACCGCGGCTGCAGCGCACCCGCGCTCTCGACC 1069
QY 721 AGGAGCTGTGCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCGCCCTCGAGGAG 780
Db 1070 AGGAGCTGTGCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCGCCCTCGAGGAG 1129
QY 781 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGGTCTCTTCACTATGTGTTCTCGCC 840
Db 1130 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGGTCTCTTCACTATGTGTTCTCGCC 1189
QY 841 GTAATTATCGCGCTTACTATGAGGATTTAAGGATGTCAAGGAGAAAACAGGACCTCT 900
Db 1190 GTAATTATCGCGCTTACTATGAGGATTTAAGGATGTCAAGGAGAAAACAGGACCTCT 1249
QY 901 GAAGAAGCAAGAACCTCGAGCCTTGGGATTTCTATCTGTGATTTCAATTGTGACCT 960
Db 1250 GAAGAAGCAAGAACCTCGAGCCTTGGGATTTCTATCTGTGATTTCAATTGTGACCT 1309
QY 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCAGAAATTTTCATT 1020
Db 1310 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCAGAAATTTTCATT 1369
QY 1021 AGACCTCTTAGGTACAGGCGGTCAGCAATTCACATAATGGAATCCAGTCTGTGA 1080
Db 1370 AGACCTCTTAGGTACAGGCGGTCAGCAATTCACATAATGGAATCCAGTCTGTGA 1429

RESULT 4

US-09-016-434-1474
; Sequence 1474, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1474:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: g940378
US-09-016-434-1474
Query Match 78.3%; Score 846; DB 4; Length 1216;
Best Local Similarity: 100.0%; Pred. No. 7.5e-200;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCGCTTCTACCGCTGCCAGAACACCACTCTGTGGAAGAAAGGCAACTCGGCG 60
Db 350 ATGAAGTCGCGCTTCTACCGCTGCCAGAACACCACTCTGTGGAAGAAAGGCAACTCGGCG 409
QY 61 GTGATGGCGGGGTGCTCTTTCAGCAACCGGCTCTTGGGCAACCTCTGTGGCCCTGGGGCTG 120
Db 410 GTGATGGCGGGGTGCTCTTTCAGCAACCGGCTCTTGGGCAACCTCTGTGGCCCTGGGGCTG 469
QY 121 CTGGCGGCTCGGGCTGGGGGTGCTGCGGGCGTCCACTGCGGCGCGCTGCGCTCGGTC 180
Db 470 CTGGCGGCTCGGGCTGGGGGTGCTGCGGGCGTCCACTGCGGCGCGCTGCGCTCGGTC 529
QY 181 TTCTACATGCTGTGTGGCTGACCGTCAACGACTTGTGGGCAAGTGCCTCTTAAGC 240
Db 530 TTCTACATGCTGTGTGGCTGACCGTCAACGACTTGTGGGCAAGTGCCTCTTAAGC 589
QY 241 CGGTGTGTGCTGCTGCTTACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCGCAATTG 300
Db 590 CGGTGTGTGCTGCTTACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCGCAATTG 649
QY 301 GACAACTGTTGTGCCAAGCCTTGGCTTCTTATCATGCTCTTTGGGCTCTCTCGACA 360
Db 650 GACAACTGTTGTGCCAAGCCTTGGCTTCTTATCATGCTCTTTGGGCTCTCTCGACA 709
QY 361 CTGCAACTCTTGGCCATGGCACTGAGTGTGGCTCTCCCTAGGCAACCTTCTTCTAC 420
Db 710 CTGCAACTCTTGGCCATGGCACTGAGTGTGGCTCTCCCTAGGCAACCTTCTTCTAC 769
QY 421 CGAGCGCACATCACCTCGGCTGGGCGCACTGTGTGGCCCGGTGGTGAAGCTTCTGAGCGCC 540
Db 770 CGAGCGCACATCACCTCGGCTGGGCGCACTGTGTGGCCCGGTGGTGAAGCTTCTGAGCGCC 829
QY 481 CTGGCTTTCTGGGCTTACCTTTCATGGGCTTGGGAAAGTTCGTGAGTACTGCGCCGCG 540
Db 830 CTGGCTTTCTGGGCTTACCTTTCATGGGCTTGGGAAAGTTCGTGAGTACTGCGCCGCG 889
QY 541 ACCTGTGCTTTATCCAGATGTCCAGAGAGGCTCGCTGTGCGGTGTGGGGTACTCT 600
Db 890 ACCTGTGCTTTATCCAGATGTCCAGAGAGGCTCGCTGTGCGGTGTGGGGTACTCT 949
QY 601 GTGCTTACTCCAGCTCATGCGCTGTGTGCTTTCGCAACCGTGTGTGCAACCTCGGC 660
Db 950 GTGCTTACTCCAGCTCATGCGCTGTGTGCTTTCGCAACCGTGTGTGCAACCTCGGC 1009
QY 661 GCCATGCGCAACCTCTATGCGATGCAACCGGCTTGGGAAAGTTCGTGAGTACTGCGCCG 720
Db 1010 GCCATGCGCAACCTCTATGCGATGCAACCGGCTTGGGAAAGTTCGTGAGTACTGCGCCG 1069
QY 721 AGGAGCTGTGCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCGCCCTCGAGGAG 780
Db 1070 AGGAGCTGTGCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCGCCCTCGAGGAG 1129
QY 781 CTGGATCACTCTGCTGCTGCGCTGATGACCGGTCTTTCACATATGTGTTCTCTGCCC 840
Db 1130 CTGGATCACTCTGCTGCTGCGCTGATGACCGGTCTTTCACATATGTGTTCTCTGCCC 1189
QY 841 GTAATT 846
Db 1190 GTAATT 1195

RESULT 5

US-08-239-431A-3
; Sequence 3, Application US/08239431A
; Patent No. 5716835
; GENERAL INFORMATION:

LOCATION: (157)...(1233)
US-09-267-423-3

Query Match 20.4%; Score 220.6; DB 3; Length 2296;
Best Local Similarity 57.8%; Pred. No. 9e-45;
Matches 557; Conservative 0; Mismatches 349; Indels 57; Gaps 7;

QY 48 AGGCAACTCGGCGGTGATGGGGGGTGTCTTTACGACCGGCGCTCTGGGCAACTGCT 107
DB 219 AGGCGAAGCCAGCCATCAGCTCGTCAITGTTCTGGCGGGGTGTGGGAACCTCAT 278

QY 108 GGCCTTGGGGCTGCTGGCGCGCTCGGGGTGGGT--GGTGTCTGGGGGTCCACTGCGC 165
DB 279 AGCACTGGCGCTGCTGGCGCGCGCTGGCGGGGAGCGTGGGTGACGCGCGCGCAG 338

QY 166 CGCTGTC--CTCGGTCTTACATGCTGTGTGGCTGACGGTCA CGCACTTGTGG 224
DB 339 GAGCTCCCTCTCTTGTTCACGCTGCTGGTTCACCGAGCTGGTTCACCGACTGCTCG 398

QY 225 CAAGTGCCTCTTAAGCCCGGTGTGCTGCTACGCTCAGAACCGGAGTCTGGGT 284
DB 399 GACCTGCTTACAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458

QY 285 GCTTGGCGCGCAATGGACAACTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
DB 459 ACTGGGCGC-----GAGAGCGCGCGTGCACCTACTTCTGCTTGGCACTGCTTCT 512

QY 345 TGGGTCTCTCGACACTGCACTCTGCGCCAGTGGAGTGTGGCTTCTGCTAGG 404
DB 513 CAGCTTGGCGCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572

QY 405 GCACCTTCTTCTACCGAGCGCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
DB 573 GCACCTTCTTCTACCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632

QY 465 GGTGAGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
DB 633 CATCTATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692

QY 525 GAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
DB 693 CCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734

QY 585 GGTGCTGGGTACTCTGCT 644
DB 735 ----GACCGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791

QY 645 GCTGTGCAACCTCGGCGCATCGCAACCTCTATGCGATGCTGCTGCTGCTGCTGCTGCT 702
DB 792 CGCTTGCACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851

QY 703 CACCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
DB 852 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911

QY 763 CTTGACCCCT----GGAGGCTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
DB 912 AAGGTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971

QY 819 CTTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
DB 972 CTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011

QY 879 CAAGGAGAAAAACAGACTCTGTAAGAACGAGAACTCTGCGAGCTTTCGATTTCTATC 938
DB 1012 -ATGAATGAACTCTTCCGAAAGAAATGAGACCTTCCAGCTCTTAGGTCTTTATC 1070

QY 939 TGTGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
DB 1071 AATTAACTAAATTAAGCCCTTGGTCTTGGCCATCTTAGCCCTCTCTGCTGCTGCTGCT 1130

QY 999 ATT 1001

DB 1131 AAT 1133

RESULT 7

US-09-016-434-1441
; Sequence 1441, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9639719
; US-09-016-434-1441

Query Match 20.3%; Score 219; DB 4; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-44;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

QY 48 AGGCAACTCGGCGGTGATGGGGGGTGTCTTTACGACCGGCGCTCTGGGCAACTGCT 107
DB 219 AGGCGAAGCCAGCCATCAGCTCGTCAITGTTCTGGCGGGGTGTGGGAACCTCAT 278

QY 108 GGCCTTGGGGGTGCTGGCGCGCTCGGGGTGGGT--GGTGTCTGGGGGTCCACTGCGC 165
DB 279 AGCACTGGCGCTGCTGGCGCGCGCTGGCGGGGAGCGTGGGTGACGCGCGCGCAG 338

QY 166 CGCTGTC--CTCGGTCTTACATGCTGTGTGGCTGACGGTCA CGCACTTGTGG 224
DB 339 GAGCTCCCTCTCTTGTTCACGCTGCTGGTTCACCGAGCTGGTTCACCGACTGCTCG 398

QY 225 CAAGTGCCTCTTAAGCCCGGTGTGCTGCTACGCTCAGAACCGGAGTCTGGGT 284
DB 399 GACCTGCTTACAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458

QY 285 GCTTGGCGCGCAATGGACAACTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344

Db 459 ACTGGGCCCC-----GAGAGCGCGGTGTCACCTACTTTCGCTTTTCGCCATGACCTTCTT 512
Qy 345 TGGGCTCTCTGACACTGCACTCTGCGCATGGCACTGGAGTGTGCTCTCCCTAGG 404
Db 513 CAGCTTGGCCAGCATGCTCTATGCTCTTGCCTATGGCCCTGGAGCGCTACTCTCGATCG 572
Qy 405 GCACCTTTCTTCTACGAGCGGCACATACCTGCGCGCTGGCGCACTGGTGGCCCCGGT 464
Db 573 GCACCTTACTTCTACAGCGCGCTCTCGGCTCCGGGGCGCTGGCGTGTGCTGT 632
Qy 465 GGTGAGCGCTTCTCTCCCTGGCTTCTGCGCGCTTACCTTTTCATGGGCTTCGGGAAGTTCGT 524
Db 633 CATCTATGAGTCTCTCTGCTCTCTGCTGCTGCGCTGTGGAATAAGGAGTACGT 592
Qy 525 GCAGTACTGCCCGGCACTGTGCTCTTATCCAGATGTGTCACGAGAGGGCTCGCTGT 584
Db 693 CCAGTACTGCCCGGCACTGTGCTCTCATCGGCACTGGCG----- 734
Qy 585 GGTGCTGGGGTACTCTGTGCTCTACTCCAGCTCATGGCGCTGCTGCTCTCGCCACCT 644
Db 735 ---GACCGCTTACCTGACGTGTACGCCACCTGCTGTCTCTCATTTGTCTCGGTGCT 791
Qy 645 GCTGTGCAACCTCGGCGCATGCGCAACTCTATGCGATGCACTGGCG--GCTGCAAGCG 702
Db 792 CGCTGCACTTCACTGCTCATTTCTCACTCATCGCATGCACTGGCGAAGCGGAGAG 851
Qy 703 CACCGCGCTCTGCACTGAGGACTGTGCGAGCGCGCGCGAAGGAGGAGCGTCC 762
Db 852 CGCTGCGGACCTTCTCCGAGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGGGA 911
Qy 763 CTTAGCCCT-----GGAGAGTGGATCACCTCTGCTGCTGCGCTGATGACCGTGT 818
Db 912 AAGGAGTCCATGGCGAGGAGACGACCATCTCATTTCTCTGCTGCTATCATGACCATCA 971
Qy 819 CTTCACTATGTCTCTCTCCCGTAATTTATCGCGTCTACTATGAGCATTTAAGGATGT 878
Db 972 CTTGCGGCTGCTCTCTGCTCTTTCAGATTTTGCATAT----- 1011
Qy 879 CAAGGAGAAAAACAGGACTCTGAAGAACGAGAACTCCGAGCGTTGCGATTTCTATC 938
Db 1012 -ATGAATGAACCTCTTCCGAAAGGAAATGGGACCTCCAAGCTCTTAGGTTTTATC 1070
Qy 939 TGTGATTTCAATGTGGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGAT 998
Db 1071 AATTAATTAATTAATGACCTTGGGTCTTTGCCATCTTAGGCTCTCTGAGACT 1130
Qy 999 ATT 1001
Db 1131 AAT 1133

RESULT 8

US-09-293-170-2
; Sequence 2, Application US/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Breyer, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; FILE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: US/09/293,170
; CURRENT FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081,989
; EARLIER FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (300)...(2126)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-09-293-170-2

Query Match 20.3%; Score 219; DB 3; Length 6446;
Best Local Similarity 57.7%; Pred. No. 3.4e-44;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

Qy 48 AGCGAACTCGGCGGTGATGGGGGGGTGCTTTAGCACCGCGCTCTCGGCAACCTGTCT 107
Db 596 AGCGAAAGCCAGCATCAGTCCGTATGTTCTCGCGCGGGGTCTCGGAGAACCTCAT 655
Qy 108 GCGCTTGGGGTGTGTCGCGCGCTCGGGGGCTGGGGT--GGTGTGCGGGGTCCACTGCGC 165
Db 656 AGCACTGGCGCTGTGGCGCGCGCTGGCGGGGAGCTGGGGGTGCAGCGCGCGCGCAG 715
Qy 166 CCGCTGCCC-CTCGGTCTTCTACATGCTGGTGTGTCGCTGACGGTCAACGACTTGTGGG 224
Db 716 GAGCTCCCTCTCTCTTGTTCACGTGCTGGTGACCGAGCTGGTGTTCACGACCTGTCTCG 775
Qy 225 CAAGTGCTCTTAAGCGCGGTGCTGCTGCTCAAGCTTTGCGCTTTCTTCTCATGTCTTCTT 284
Db 776 GACCTGCTCTATCAGCCAGTGTACTGCTTGTGATCGCGCGAACCAGACCTGTGTGGC 835
Qy 285 GCTTGGCGCGCATTTGGCAACTCGTGTGTGCAAGCTTTGCGCTTTCTTCTCATGTCTTCTT 344
Db 836 ACTGGCGCCC-----GAGAGCGCGGTGACCTACTTTGCTTTTCGCCATGACCTTCTT 889
Qy 345 TGGGCTCTCTCGACACTGTGCAACTCTGTGGCACTGGCACTGGAGTGTGCTCTCCCTAGG 404
Db 890 CAGCCTGGCCACGATGCTCTCTTCCCATGTCCTCTGGAGCGCTACTCTCTCGATCGG 949
Qy 405 GCACCTTTTCTTCTACGAGCGGCAATCACCTGCGCTGCGCGCGCACTGTGCGCCCCGGT 464
Db 950 GACCCCTCTACTTCTACAGCGCGCGCTCTGCGCTCTCGGGGGCGCTGCGCTGTCTGTCTGT 1009
Qy 465 GGTGAGCGCTTCTCTCGCTTTCTGCGCTACTCTTTTCATGGGCTTCGGGAAGTTCGT 524
Db 1010 CATCTATGAGTCTCCCTGCTCTCTCTGCTGCTGCGCTGTGGACTATGGGAGTACGT 1069
Qy 525 GCAGTACTGCCCCGCGCACTGTGCTTTTATCCAGATGTCTCAGAGAGGGCTCGCTGTCTC 584
Db 1070 CCAGTACTGCCCCGCGGACCTGTGTCTTCTATCGGCACTGGGG----- 1111
Qy 585 GGTGCTGGGGTACTCTGTGCTCTACTCCAGCTCATGGCGCTGCTGGTCTCTCGCCACCT 644
Db 1112 ---GACCGCTTACTGCGAGCTGTACGCCACCTGCTGTGCTTCTCATTTGTCTCGGTGT 1168
Qy 645 GCTGTGCAACCTCGGCGCATGCGCAACTCTATGCGATGCACTGGCG--GCTGAGCGG 702
Db 1169 CGCTGCAACTTCAGTGTCTTCTCAACTCATCGCATGCACTGGCGAAGCGGAGAG 1228
Qy 703 CACCGCGCTCTGCACTGAGGAGCTGTGCGAGCGCGCGCGGAGCGGAGGAGGAGCTCC 762
Db 1229 CCGCTGCGGACCTTCTCTGGGAGTGGCGGGCGCGCGCGGGCGCGCGGAGGAGGGA 1288
Qy 763 CTTAGCCCCCT-----GGAGAGCTGGATCAGCTCTGCTGCTGCGCTGATGACCGTGTCT 818
Db 1289 AAGGAGTGTCCATGGCGGAGGAGACGACCTCATTTCTCTGGGTATCATGACCATCA 1348
Qy 819 CTTCACTATGTGTTCTCTGCGCGCTAATTTATCGCGCTTACTATGAGGCAATTTAAGGATGT 878
Db 1349 CTTGCGCGTCTGCTCTTTCCTTTCAGCATTTTTCATAT----- 1388
Qy 879 CAAGGAGAAAAACAGGACTCTGGAAGAGGAGAGACTCTCGAGCTCTGCGATTTCTATC 938
Db 1389 -ATGAATGAACCTCTTCCGAAAGGAAATGGGACCTCCAAGCTCTTAGGTTTTATC 1447
Qy 939 TGTGATTTCAATGTGAGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGAT 998
Db 1448 AATTAATTAATTAATGACCTTGGGTCTTTGCCATCTTAGGCTCTCTGCTTCTGAGACT 1507

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-29

Query Match 19.5%; Score 211; DB 2; Length 1074;

Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

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QY 48 AGGCAACTCGGCGGTGATGGCGGGTGTCTTTCAGACCGGCTCTCTGGCAACTGTCT 107
DB 63 AGCGGAAGCCAGCCATCAGTTCCTCATGTTCTCGCGGGTGTCTGGGAACTCAT 122
QY 108 GGCCTTGGGGTGTCTGGCGGTCTGGGGTGGGGT--GGTGTCTGGGGTCTCACTGC 165
DB 123 AGAACTGGCGGTCTGGCGCGGTCTGGCGGGGACGTGGGTGTCAGCGCGCGGTAG 182
QY 166 CGCTGCC--CTGGGTCTTCTACATGCTGTGTGTGCGCTGACGGTCACCGACTTGTGG 224
DB 183 GAGCTCCCTCTCTTGTTCACAGTGTGTGTGACCGAGCTGGTGTTCACCGACTTGT 242
QY 225 CAAGTGCCTCTTAAGCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 243 GACCTGCTTCATCAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
QY 285 GCTTGGCGCGCATTTGGAACAACCTGTTGTGCCAAGCTTTTCCCTTCTTCTTCTT 344
DB 303 ACTGGCGCC-----GAGAGCGCGCTCCACCTACTTTCGCTTTCGCGCATGAC 356
QY 345 TGGGCTCTCTTGACACTGAACTCTTGGCATGGAAGTGTGTGTGTGTGTGTGTGTGT 404
DB 357 CAGCTTGGCGCATGCTCATGCTTTCACCATGGCTTGGAGCGCTACTCTTCGATCG 416
QY 405 GCACCTTCTTCTACCGAGCGCACATCACCCTGCGCTGGCGCACTGTGGCGCCGCT 464
DB 417 GCACCTTCTTCTACCGAGCGCGCTCTCGCGCTCCGGCGCGCTGGCGGTGTGTGTGT 476
QY 465 GGTGAGCGCTTCTTCTCGCTTCTTCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCT 524
DB 477 CATCTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 536
QY 525 GAGTACTGCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
DB 537 CCAGTACTGCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 578
QY 585 GGTGTGGGGTACTCTGTGTCTTCTTCTGAGCTTCTGAGCTTCTGCTGCTTCTGCT 644
DB 579 ---GACCGCTTACCTGACGTGTACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCT 635
QY 645 GCTGTGCAACCTCGGCGCATCGCAACCTCTATGGATGACACCGGCG--GCTGACGCG 702
DB 636 CGCTTGCACTTCACTGTGTCTTCTCACTCTCATCTGCTGCTGCTGCTGCTGCTGCT 695
QY 703 CACCGCGCTCTTGCAACGAGGACTGTGTCGAGCGCGCGCGGAGCGGAGGAGGAGG 762
DB 696 CGCTGCGGACCTTCTCTGCGAGTGTGGCGGGGCGCGCGCGCGCGCGCGCGCGCG 755
QY 763 CTTACGCCCT---GGAGGAGTGTGATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 818
DB 756 AAGGTGTCCATGGCGGAGGAGACGACCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCT 815
QY 819 CTTTCACTATGTGTCTCTCGCGCTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGT 878
DB 816 CTTGCGCGCTGCTCTCTGCTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 855
QY 879 CAAAGGAGAAAAACAGGACTCTTGAAGAGCAGAACCTTCCGAGCTTCCGATTTCTAT 938
DB 856 -ATGAATGAACCTCTTCCCGAAGGAAAAATGGGACCTTCCAAGCTTCTTAGGTTTATC 914
QY 939 TGTGATTTCAATTTGGACCTTGGATTTTATCATTTTTCAGATCTTCCAGTATTTCCGAT 998
DB 915 AATTAATTAATTAATTTGGGCTTGTGCGCTTCTTGGCCCTTCTTCTGAGACT 974
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QY 999 ATT 1001
DB 975 AAT 977

RESULT 11

US-08-461-379A-29
; Sequence 29, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Preestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; APPLICATION NUMBER: & 07/796,066
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)470-0700
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-461-379A-29

Query Match 19.5%; Score 211; DB 2; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

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QY 48 AGGCAACTCGGCGGTGATGGCGGGTGTCTTTCAGACCGGCTCTCTGGCAACTGTCT 107
DB 63 AGCGGAAGCCAGCCATCAGTTCCTCATGTTCTCGCGGGTGTCTGGGAACTCAT 122
QY 108 GGCCTTGGGGTGTCTGGCGGTCTGGGGTGGGGT--GGTGTCTGGGGTCTCACTGC 165
DB 123 AGAACTGGCGGTCTGGCGCGGTCTGGCGGGGACGTGGGTGTCAGCGCGCGGTAG 182
QY 166 CGCTGCC--CTCGGTCTTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 224
DB 183 GAGCTCCCTCTCTTGTTCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 242
QY 225 CAAGTGCCTCTTAAGCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 243 GACCTGCTTCATCAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
QY 285 GCTTGGCGCGCATTTGGAACAACCTGTTGTGCCAAGCTTTTCCCTTCTTCTTCTT 344
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Db 303 ACTGGCGCC-----GAGAGCGCGCTCCACCTACTTCGCTTCGCGCATGACCTTCTT 356
Qy 345 TGGGCTCTCTCGACACTGCAACTCTGCGCATGCACTGGAGTGTGCTCTCCCTAGG 404
Db 357 CAGCTGGCGCAGATGCTCATGCTCTTCCACCATGCGCTGGAGCGCTACCTCTCGATCGG 416
Qy 405 GCACCTTTCTTCTACCGACGACATACCTGCGCTGGCGGCGACTGTTGGCGCCCGGT 464
Db 417 GCACCTTACTTCTACCGCGCGGCTCTGCGCTCGGCGGCGCTGCGCTGCTGCTGT 476
Qy 465 GGTGAGCGCTTCTCTGCGCTTCTGCGGCTACTTTCATGGGCTTCGGAAAGTTCGT 524
Db 477 CATCTATGAGTCTCTCTCTCTGCTCACTGCGCTGCTGCACTATGGGCGAGTACGT 536
Qy 525 GCAGTACTGCGCGGCGACCTGCTTTCATCAGATGCTCCAGAGGCGGCTGCTGTC 584
Db 537 CCAGTACTGCGCGGCGACCTGCTGCTTCATCGGCGCGG----- 578
Qy 585 GGTGCTGGGCTACTCTGCTCTACTCCAGCTCATGCGCTGCTGCTGCTCGCACCGT 644
Db 579 ---GACCGCTTACCTGAGCTGTACGCCACCTGCTGCTGCTCTCATGTTCTCGGTGT 635
Qy 645 GCTGTGCAACTCGGCGCATCGCAACTCTATGCGATGCAACCGCG--GCTGAGCGG 702
Db 636 CGCTGCAACTTCAGTGTCTATTCACCTCATCGCATGCAACCGCGAAGCGGAGAAG 695
Qy 703 CACCGCGCTCTGACACGAGGACTGTGCGAGCGCGCGCGGAGGAGGAGGTC 762
Db 696 CGCTGCGGACCTTCTGCGGAGTGGCGGCGCGCGCGCGCGCGCGGAGGAGG 755
Qy 763 CTTGAGCCCT---GGAGGAGTGCATCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 756 AAGGTGTCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 815
Qy 819 CTTCACTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
Db 816 CTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
Qy 879 CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 938
Db 856 -ATGAATGAACCTCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 914
Qy 939 TGTGATTTCAATTTGGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTTGGAT 998
Db 915 AATTATTCATTAATGACCTTGGTCTTGCCATCTTGGATCTTGGATCTTGGATCT 974
Qy 999 ATT 1001
Db 975 AAT 977

RESULT 12

US-08-462-390B-29
Sequence 29, Application US/08462390B
Patent No. 5892894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ADDRESS: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Qy 48 AGGCAACTCGGCGGTGATGGCGGCTGCTCTTACAGCACCGGCTCTCTGGGCAACTGCT 107
Db 63 AGGCGAAGAGCCAGCCATCAGTTCGCTCATGTTCTCGGCGCGGCTGCTGGGAACTCAT 122
Qy 108 GCGCTGCGGCTGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 165
Db 123 AGAATGCGCTGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 182
Qy 166 CCGCTGCGC-CTCGGCTCTTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
Db 183 GAGCTCCCTCTCTGTTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
Qy 225 CAAAGTCTCTTAAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 284
Db 243 GACCTGCTCATCAGCCAGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302
Qy 285 GCTTGGCGCGGATGGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
Db 303 ACTGGCGCC-----GAGAGCGCGCGTCCACCTACTTTCGCTTTCGCGCATGACCTTCT 356
Qy 345 TGGGCTCTCTCGACACTGCAACTCTGCGCCATGCACTGAGAGTGTGCTGCTCTCGCTAGG 404
Db 357 CAGCTGCGCAGGATGCTCATGCTTTCACCATGCGCTTGGAGCGCTACCTCTCGATCGG 416
Qy 405 GCACCTTTTCTTCTACCGACGCGCATACCTGCTGCGCTGCGCGCATGCTGCTGCGCGCT 464
Db 417 GCACCTTCTTCTTCTACCGACGCGCGCTGCTGCGCTGCGCGCGCTGCTGCTGCTGCT 476
Qy 465 GGTGAGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
Db 477 CATCTATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536
Qy 525 GCAGTACTGCGCGCGCACTGCTGCTTTCATCAGATGCTTTCACAGAGGAGGCTGCTGCT 584
Db 537 CCAGTACTGCGCGGCGACCTGCTGCTTTCATCGGCGCGGCG----- 578
Qy 585 GGTGCTGGGCTACTCTGCTGCTTCTACTCCAGCTCATGCGCTGCTGCTGCTGCTGCTGCT 644
Db 579 ---GACCGCTTACCTGAGCTGTACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
Qy 645 GCTGTGCAACTCGGCGCATGCGCAACTCTATGCGATGCAACCGCG--GCTGAGCGG 702
Db 636 CGCTGCAACTTCAGTGTCTATTCACCTCATCGCATGCAACCGCGAAGCGGAGAAG 695

US-08-465-585C-29
; Sequence 29, Application US/08465585C
; Patent No. 6027914
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 900071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,585C
; FILING DATE: 5-JUNE-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-465-585C-29

Query Match 19.5%; Score 211; DB 3; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

QY	48	AGGCACTCGGCGGTGATGGCGGGTGTCTTACGACCGCGCTCTGGGCAACTGCT	107
DB	63	AGCGAAGACCCAGGACATCAGTTCGTGATGTTCTGCGCGGGGTGCTGGGAACTCAT	122
QY	108	GGCCCTCGGCGGTGCTGGCGCGCTCGGGGTGGGT--GGTGTGCGCGGCTCCACTGCGC	165
DB	123	AGAACTGGCGCTGTGGCGCGCGCTGGCGAGGGGACGTGGGGTCAGCGCGCGGTAG	182
QY	166	CGCTGCCC-CTGGTCTTCTACATGCTGTGTGTGGCTGACGGTACCGACTTGTGTGG	224
DB	183	GAGCTTCCTCTCTGTTCCAGGTGTGTGTGACCGAGCTGGTGTTCACCGACCTGCTCG	242
QY	225	CAAGTGCCTCTAAGCCCGGTGTGTGCTGCTGCTAGCTCAGAACCGAGTCTGGGT	284
DB	243	GACCTGCTCATAGCGCCAGTGGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	302
QY	285	GCTTGGCGCGGATGGACAACTCGTGTGTGCGCAAGCTTTCGCTTCTTCTCATGCTCTT	344
DB	303	ACTGGGCGCC-----GAGAGCGCGCGTCCACTTCTGCTTTCGCTGACCTTCTT	356
QY	345	TGGGTCTCTCTGACACTGCTGCGCACTGCTGCGCACTGGCACTGGAGTGTGCTCTCTC	404
DB	357	CAGCTGGCCAGGATGCTCATGCTCTTCACTTCACTGCGCTGGAGCGCTACCTCTCTG	416

QY	405	GCACCCCTTCTTCTTACCGACCGCACATCACCTCGCGCTCGCGCGCACCTGGTGGCCCCCGGT	464
DB	417	GCACCCCTTCTTCTTACCGACCGCGCGGTCTCGGGTCCGGGGCGCTGGCGGTGCTGCTGCT	476
QY	465	GGTGAAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	524
DB	477	CATCTATGCACTCTCCCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	536
QY	525	GCAGTACTGCCCCCGGCACTTGTGCTTATCCAGATGTTTATCCAGAGGAGGCTGCTGCTGTC	584
DB	537	CCAGTACTGCCCCCGGCACTTGTGCTTATCCAGATGTTTATCCAGAGGAGGCTGCTGCTGTC	578
QY	585	GGTGTGGGTACTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	644
DB	579	---GACCGCTTACCTGCACTGTAGCGCACCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCT	635
QY	645	GCTGTCAACCTCGCGCGCATGCGCAACTCTTATGCGATGACCGCGG--GCTGCGCGG	702
DB	636	CGCTGCAACTTCACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	695
QY	703	CACCGCGCTCTGCAACCGAGGACTGTGCGGAGCGCGCGCGGCGGAGGAGGAGGAGGAGGAGG	762
DB	696	CGCTGCGGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	755
QY	763	CCTCAGCCCTT---GGAGGAGCTGGATCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	818
DB	756	AAGGTGTCTATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	815
QY	819	CTTCACTATGTTCTTCTGCGGTAATTTATGCGGCTTATGCGGCTTATGAGGATTTAAGGATGT	878
DB	816	CTTCTGCGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	855
QY	879	CAAGGAGAAACAGGACCTCTGAGAGCAGAGACCTCCGAGCCTTCCGAGCTTTCGATTTCTATC	938
DB	856	-ATGAATGAACCTTCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	914
QY	939	TGTGATTTCAATTTGGACCTTGGATTTTATCATTTTATCATTTTATCATTTTATCATTTTATC	998
DB	915	AATTAATTCATTAATGACCTTGGTCTTTGGCATCTTAGGCTCTTAGGCTCTTCTTCTGAGCT	974
QY	999	ATT 1001	
DB	975	AAT 977	

RESULT 15
US-08-652-446-29
; Sequence 29, Application US/08652446
; Patent No. 6057427
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRS
; TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,446
; FILING DATE:
; PRIOR APPLICATION DATA:

444 South Flower St. - Suite 1900

APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-652-446-29

Query Match 19.5%; Score 211; DB 3; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;
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DB 63 AGGCGAAAGCCAGCCATCAGTTCCGTCATGTTCTCGGCGGGGTGCTGGGAAACCTCAT 122
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DB 123 AGAATGCGGCTGCTGGGCGGCGGTGGGAGGGGACGTGGGTGCGAGCGCGGCGGTAG 182
QY 166 CCGCTGCC-CTGCGTCTTTACATGCTGGTGTGTGGCCTGACGGTCAACCGACTTGTCTGGG 224
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QY 585 GGTGTGGGGTACTCTGTGCTCTACTCCAGCCTCATGGGCTGCTGGTCTCTGCCACCGT 644
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QY 645 GCTGTGCAACCTCGCGCCATCGCAACCTCTATGCGATGCAACCGCG--GTCGACGCG 702
Db 636 CGCCTGCAACTTCAGTGTCTATTTCTCAACCTCATCCGATGCAACCGCGGAGAG 695
QY 703 CACCGCGCTCTCGACACGAGGACTGTGCGAGCGCGCGGACCGGAGGGAGGCTGCC 762
Db 696 CCGCTCGGACCTTCCCTGGGCACTGGCGGGCGGCGCCCGGGCGCGGAGAGGGA 755
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Db 975 AAT 977

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Job time : 208.43 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 15:32:17 ; Search time 712.004 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1253	US-10-276-774-1020	Sequence 1020, App
2	1080	100.0	1253	US-10-128-558-263	Sequence 263, App
3	900.4	83.4	1505	US-10-128-558-24	Sequence 24, App1
4	846	78.3	1216	US-10-305-720-1474	Sequence 1474, App
5	829	76.8	964	US-10-029-386-24136	Sequence 24136, A
6	829	76.8	964	US-10-029-386-10081	Sequence 10081, A
7	436	40.4	597	US-10-225-567A-286	Sequence 286, App
8	436	40.4	597	US-10-029-386-23781	Sequence 23781, A
9	220.6	20.4	2395	US-10-108-714-3	Sequence 3, App1
10	220.6	20.4	2395	US-10-684-206-37	Sequence 37, App1
11	219	20.3	2372	US-10-225-567A-290	Sequence 290, App

12	219	20.3	2372	17	US-10-352-684A-35	Sequence 35, App1
13	219	20.3	2372	17	US-10-366-288-35	Sequence 35, App1
14	219	20.3	2372	17	US-10-305-720-1441	Sequence 1441, App
15	219	20.3	2372	18	US-10-755-889-91	Sequence 91, App1
16	219	20.3	6446	17	US-10-139-686A-2	Sequence 2, App1
17	214.2	19.8	1077	10	US-09-826-509-558	Sequence 558, App
18	214.2	19.8	1077	16	US-10-925-095-558	Sequence 558, App
19	208	19.3	501	16	US-10-029-386-10432	Sequence 10432, A
20	203.4	18.8	2824	17	US-10-108-260A-1464	Sequence 1464, App
21	201.8	18.7	1417	17	US-10-305-720-1403	Sequence 1403, App
22	201.8	18.7	1417	17	US-10-225-567A-284	Sequence 284, App
23	200.6	18.6	1360	9	US-09-917-800A-1482	Sequence 1482, App
24	186.4	17.3	1342	9	US-10-349-528-3	Sequence 3, App1
25	108.8	10.1	1209	18	US-10-472-362-2	Sequence 2, App1
26	108.8	10.1	1209	18	US-10-681-029-7	Sequence 7, App1
27	108.8	10.1	3918	9	US-09-781-311-1	Sequence 1, App1
28	107.2	9.9	1140	19	US-10-681-029-1	Sequence 1, App1
29	107.2	9.9	1209	19	US-09-826-509-556	Sequence 556, App
30	107.2	9.9	1376	15	US-10-925-095-556	Sequence 556, App
31	107.2	9.9	1376	15	US-10-225-567A-288	Sequence 288, App
32	107.2	9.9	1376	17	US-10-305-720-1361	Sequence 1361, App
33	107.2	9.9	1376	18	US-10-473-974-179	Sequence 179, App
34	107.2	9.9	1473	14	US-10-243-501-1	Sequence 1, App1
35	107.2	9.9	1473	14	US-10-243-501-2	Sequence 2, App1
36	103.4	9.6	1473	14	US-10-243-351-1	Sequence 1, App1
37	101.2	9.4	1467	19	US-09-826-509-560	Sequence 560, App
38	101.2	9.4	1467	19	US-10-925-095-560	Sequence 560, App
39	101.2	9.4	1554	15	US-10-320-351-1	Sequence 1, App1
40	101.2	9.4	1554	15	US-10-320-351-2	Sequence 2, App1
41	101.2	9.4	1558	15	US-10-225-567A-295	Sequence 295, App
42	101.2	9.4	1558	17	US-10-295-027-1180	Sequence 1180, App
43	101.2	9.4	1558	17	US-10-305-720-1389	Sequence 1389, App
44	101.2	9.4	1558	18	US-10-755-889-169	Sequence 169, App
45	101.2	9.4	1558	18	US-10-755-889-169	Sequence 38, App1

ALIGNMENTS

RESULT 1
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; Sequence 1020, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1020
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-276-774-1020

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Best Local Similarity 100.0%; Pred. No. 2.5e-306;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 122 ATGAAGTCGCGGTCCTTACGCGTCCAGAACACACCTCTGTGAAAGCAACTGCGG 181
QY 61 GTGAATGGGCGGGGTCCTTACGCGTCCAGAACACCGGCTCTGTGGAACCTGCGGCGCTG 120
DB 182 GTGAATGGGCGGGGTCCTTACGCGTCCAGAACACCGGCTCTGTGGAACCTGCGGCGCTG 241

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QY 121 CTGGCGGCTCGGGGCTGGGGTGTGCTGCGCGCTGCACTGCGCCCGCTCGCTG 180
DB 242 CTGGCGGCTCGGGGCTGGGGTGTGCTGCGCGCTGCACTGCGCCCGCTCGCTG 301
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DB 302 TTCTACATGCTGTGTGTGTGCTGACGCTGCACTGCTGGGCAAGTCTCTTAAGC 361
QY 241 CCGGTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 300
DB 362 CCGGTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 421
QY 301 GACAACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
DB 422 GACAACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 481
QY 361 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 420
DB 482 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 541
QY 421 CGACGGCAATCACTCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
DB 542 CGACGGCAATCACTCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 601
QY 481 CTGGCTTTCTGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 540
DB 602 CTGGCTTTCTGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 661
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DB 662 ACCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 721
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RESULT 2
US-10-128-558-263
; Sequence 263, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei

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; APPLICANT: Weng, Gezh
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pc_fl_genes Version 6.0
; SEQ ID NO 263
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-128-558-263

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Query Match 100.0%; Score 1080; DB 18; Length 1253;
Best Local Similarity 100.0%; Pred. No. 2,5e-306;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAGTCCGCGTTCTTCACTGCTGCGCAACACACCTCTGTGGAAGAAAGCACTCGG 60
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QY 61 GTGATGGGGGGGGTGTCTTCAAGACCGGCTCTGCGGCAACCTGTGCGCCCTGGGGCTG 120
DB 182 GTGATGGGGGGGGTGTCTTCAAGACCGGCTCTGCGGCAACCTGTGCGCCCTGGGGCTG 241
QY 121 CTGGCGGCTCGGGGCTGGGGTGTGCTGTGCGGCTGCACTGCGCCGCTGCTGTGCTG 180
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Db 1142 AGACCTCTTATGATGAG 1201

RESULT 3
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; Sequence 24, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Dymnac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800

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QY 421 CGACGCGCATATCACCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 480
Db 651 CGACGCGCATATCACCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 710
QY 481 CTGCGCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 711 CTGCGCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
QY 541 ACCTGCTTTCATCCAGATGCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 771 ACCTGCTTTCATCCAGATGCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
QY 601 GTGCTTTCATCCAGCTTCATGAGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 831 GTGCTTTCATCCAGCTTCATGAGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
QY 661 GCCATGCGCAACCTTCATGAGTGCACCGCGCTGAGCGGACCCGCTGCTGCTGCTGCT 720
Db 891 GCCATGCGCAACCTTCATGAGTGCACCGCGCTGAGCGGACCCGCTGCTGCTGCTGCT 950
QY 721 AGGAGCTGTCGCGAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 951 AGGAGCTGTCGCGAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
QY 781 CTGATCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

Query Match 83.4%; Score 900.4; DB 18; Length 1505;
Best Local Similarity 89.3%; Pred. No. 1,5e-253;
Matches 1034; Conservative 0; Mismatches 1; Indels 123; Gaps 1;
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pc_fl_genes Version 6.0
; SEQ ID NO 24
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(1505)
US-10-128-558-24

Db 1011 CTGATCACCCTCTCTCTGCGGCTGANGACCGTCTCTTCACTAATGTTCTCTGCC 1070
QY 841 GTAATT----- 846
Db 1071 GTATTTGTAGTCCCGGCGCCGAGGACGACGAGCACTGACTGCGCGCGGATG 1130
QY 847 ----- 846
Db 1131 CGGCGCGGGAAGGTGAGCGATCGGATGACGCGCGCCGACGAGCTGCGCCTG 1190
QY 847 -----TATGCGCCTTACTATGAGCATTTAAGATGTCAGAGAGAAAACAGAC 897
Db 1191 GCCAGAGATGTCGCGCTTATCTATGAGCATTTAAGATGTCAGAGAGAAAACAGAC 1250
QY 898 TCTGAAGACGAGAACCTCCGAGCTTGCGATTTCTATCTGATTTCAATTGAGAC 957
Db 1251 TCTGAAGACGAGAACCTCCGAGCTTGCGATTTCTATCTGATTTCAATTGAGAC 1310
QY 958 CCTGGATTTTATCATATTTTCAGATCTCAGATATTTGAGATATTTTTCACAAAGATTTC 1017
Db 1311 CCTGGATTTTATCATATTTTCAGATCTCAGATATTTGAGATATTTTTCACAAAGATTTC 1370
QY 1018 ATTAGACCTCTTAGCTAC 1035
Db 1371 ATTAGACCTCTTAGCTAC 1388

RESULT 4

US-10-305-720-1474
Sequence 1474, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1474
LENGTH: 1216
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g940378
US-10-305-720-1474

Query Match 78.3%; Score 846; DB 17; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.3e-237;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTGCCTGCTTCTACCGCTGCGAAGAACACCACTCTGTGAAAAAGCAACTGCGCG 60
Db 350 ATGAGTGCCTGCTTCTACCGCTGCGAAGAACACCACTCTGTGAAAAAGCAACTGCGCG 409
QY 61 GTGATGCGGCGGCTGCTTCAACGACCGCTCTGCGCAACTGCTGCGCCCTGCGGCTG 120
Db 410 GTGATGCGGCGGCTGCTTCAACGACCGCTCTGCGCAACTGCTGCGCCCTGCGGCTG 469
QY 121 CTGCGCGCTGCGGCTGCGGCTGCTGCGCGGCTGCACTGCGCGCGCTGCGCTGCGTC 180
Db 470 CTGCGCGCTGCGGCTGCGGCTGCTGCGCGGCTGCTGCGCGCTGCGCGCTGCGCTG 529
QY 181 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 530 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
QY 241 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 590 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649

QY 301 GACAACTGCTTGCCCAAGCCTTGCGCTTCTTCAATGCTTCTTGGGCTCTCTGAGCA 360
Db 650 GAACTGCTTGCCCAAGCCTTGCGCTTCTTCAATGCTTCTTGGGCTCTCTGAGCA 709
QY 361 CTGCAACTCTGCGCAATGCACTGAGTGTGCTCTCTCTAGGGGCACTTCTTCTAC 420
Db 710 CTGCAACTCTGCGCAATGCACTGAGTGTGCTCTCTCTAGGGGCACTTCTTCTAC 769
QY 421 CGACGCAATCACTGCGCTGCGGCGCACTGAGTGTGCGGCGGCTGAGCGCTTCTCC 480
Db 770 CGACGCAATCACTGCGCTGCGGCGCACTGAGTGTGCGGCGGCTGAGCGCTTCTCC 829
QY 481 CTGCGCTTCTGCGCGCTACCTTTCATGAGCTTGCGGAACTTGTCAGTACTGCCCG 540
Db 830 CTGCGCTTCTGCGCGCTACCTTTCATGAGCTTGCGGAACTTGTCAGTACTGCCCG 889
QY 541 ACTGCTGCTTATTCAGATGCTTCAACGAGAGGCTGCTGCTGCTGCTGCTGCTG 600
Db 890 ACTGCTGCTTATTCAGATGCTTCAACGAGAGGCTGCTGCTGCTGCTGCTGCTG 949
QY 601 GTGCTTACTCAGGCTCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 950 GTGCTTACTCAGGCTCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009
QY 661 GCCATGCGCAACCTCTATGCGATGACCGCGCGCTGCGACCGGCACTGCTGCGAC 720
Db 1010 GCCATGCGCAACCTCTATGCGATGACCGCGCGCTGCGACCGGCACTGCTGCGAC 1069
QY 721 AAGGACTGCGCGAGCGCGCGCGCGCGAGAGGAGAGCTCCCTTCAGGCTTGAAGAG 780
Db 1070 AAGGACTGCGCGAGCGCGCGCGCGCGAGAGGAGAGCTCCCTTCAGGCTTGAAGAG 1129
QY 781 CTGATACCTCTGCTGCTGCGCTGAGTACCGTCTTCACTATGTTCTGCGCC 840
Db 1130 CTGATACCTCTGCTGCTGCGCTGAGTACCGTCTTCACTATGTTCTGCGCC 1189
QY 841 GTAATT 846
Db 1190 GTAATT 1195

RESULT 5

US-10-029-386-24136/c
Sequence 24136, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEWICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24136
LENGTH: 964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL355833.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
OTHER INFORMATION: EST_HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 1.00e-128
OTHER INFORMATION: NT HIT: U13132.1, EVALUATE 0.00e+00
US-10-029-386-24136

Query Match 76.8%; Score 829; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy		18	CGCGGCCAGAAACACCACTGTGTAATAAAGCAAACCTGGCGGATGAATGGGGGGTGT	77
Dd		964	C CGCTCCAGAACCACTCTGTGTAATAAAGCAAACCTGGCGGATGAATGGGGGGTGT	905
Oy		78	CTTCAGCACCGGCCTCTTGCGGCAACTGTGCGCCTCGGAGCTGTGCGCGCT	137
Dd		904	CTTCAGCACCGGCCTCTTGCGGCAACTGTGCGCCTCGGAGCTGTGCGCGCT	845
Oy		138	GGGGGTGTGTCTGCGGGCGTCCA CTGCGCCCCGTGCTTGTCTTCTCATGTCTGTGTG	197
Dd		844	GGGGGTGTGTCTGCGGGCGTCCA CTGCGCCCCGTGCTTGTCTTCTCATGTCTGTGTG	785
Oy		198	TGGCCTGACGGGTCA CCGA CTGCTGGAGCAAGTGCCTCCATAAGCCCCGGATGCTGAGCTGC	257
Dd		784	TGGCCTGACGGGTCA CCGA CTGCTGGAGCAAGTGCCTCCATAAGCCCCGGATGCTGAGCTGC	725
Oy		258	CTACGCTCAGAAACCGAGTCTTGCGGGTGTCTTGCGGCCGATTTGACAACCTCGTGTGCCA	317
Dd		724	CTACGCTCAGAAACCGAGTCTTGCGGGTGTCTTGCGGCCGATTTGACAACCTCGTGTGCCA	665
Oy		318	AGCCTTGCGCCTTCTTCATGTCTCTTTGGGCTCTCTCGACACTGCAACTCTCGGCAT	377
Dd		664	AGCCTTGCGCCTTCTTCATGTCTCTTTGGGCTCTCTCGACACTGCAACTCTCGGCAT	605
Oy		378	GGCACTGAGAGTGGGCTCTCCCTTAGGGACA CCCTTCTTCACAGACGGACATCAACCCT	437
Dd		604	GGCACTGAGAGTGGGCTCTCCCTTAGGGACA CCCTTCTTCACAGACGGACATCAACCCT	545
Oy		438	GCGCGCTGGGCGCACTGTGGCCCCCGGTGTGAGCGCCTTCTTCCTGCTTCTGTGCGCT	497
Dd		544	GCGCGCTGGGCGCACTGTGGCCCCCGGTGTGAGCGCCTTCTTCCTGCTTCTGTGCGCT	485
Oy		498	ACCTTTTATGGGCTTCTGGGAAATTGTGTGATGATCTGCCCCGGACACTGTGTGTTATCA	557
Dd		484	ACCTTTTATGGGCTTCTGGGAAATTGTGTGATGATCTGCCCCGGACACTGTGTGTTATCA	425
Oy		558	GATGGTCCACGAGAGGAGCTGCTGTGCGTGTGGGATCTGTGCTCTACTCAGGCT	617
Dd		424	GATGGTCCACGAGAGGAGCTGCTGTGCGTGTGGGATCTGTGCTCTACTCAGGCT	365
Oy		618	CATGGCGCTGTGCTCTCGCCACCGTGTGTGCAACTCGGCGCATGCGCAACTCTTA	677
Dd		364	CATGGCGCTGTGCTCTCGCCACCGTGTGTGCAACTCGGCGCATGCGCAACTCTTA	305
Oy		678	TGCGATGACACCGGCGCTGCGACCGGCAACCGGCTCTCTGCAACAGGACTGTGCGGAACC	737
Dd		304	TGCGATGACACCGGCGCTGCGACCGGCAACCGGCTCTCTGCAACAGGACTGTGCGGAACC	245
Oy		738	GCGCGCGGACCGGAGGAGAAGCGTCCCTCAGCGCCCTGAGAGAGCTGATCACTCTCTCT	797
Dd		244	GCGCGCGGACCGGAGGAGAAGCGTCCCTCAGCGCCCTGAGAGAGCTGATCACTCTCTCT	185
Oy		798	GCTGGCGGTGATGACCGTGTCTTTCATGTGTGTTCTGTCCCGTAAT	846
Dd		184	GCTGGCGGTGATGACCGTGTCTTTCATGTGTGTTCTGTCCCGTAAT	136

RESULT 6
US-10-029-386-10081
; Sequence 10081, Application US/10029386
; Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

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/ SEQ ID NO 10081
/ LENGTH: 597
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR14.3
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: NT HIT: U31332.1, EVALUE 0.00e+00
/ OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUE 1.00e-108
/ OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUE 1.00e-92
US-10-029-386-10081

Query Match          54.5%; Score 589; DB 16; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.9e-162;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CTACGCTCAGAAACCGAGTCTGCGGGTGTCTTGCCGCCCGCATTTGACAACTGTTGGCCA 317
DB 1 CTACGCTCAGAAACCGAGTCTGCGGGTGTCTTGCCGCCCGCATTTGACAACTGTTGGCCA 60
QY 318 AACCTTCGGCTTCTTATGTCCTTCTTTGGGCTCTCTCCGACATCGCAACTCCTGGCCAT 377
DB 61 AACCTTCGGCTTCTTATGTCCTTCTTTGGGCTCTCTCCGACATCGCAACTCCTGGCCAT 120
QY 378 GGCACCTGAGTGTGCTGCTCTCCCTAGGGGACCTTTCTTTCACGAGGACATCACTCCT 437
DB 121 GGCACCTGAGTGTGCTGCTCTCCCTAGGGGACCTTTCTTTCACGAGGACATCACTCCT 180
QY 438 GGGCTGGGCGCATGCTGTGGCCCCCGGTGTGAGGCGCTTCTCCCTGGCTTTCTGCGGCT 497
DB 181 GGGCTGGGCGCATGCTGTGGCCCCCGGTGTGAGGCGCTTCTCCCTGGCTTTCTGCGGCT 240
QY 498 ACCCTTTCATGGGCTTTGGGAAAGTTCTGTGACGATCTGCCCCGGGACACTGTGTTATCCA 557
DB 241 ACCCTTTCATGGGCTTTGGGAAAGTTCTGTGACGATCTGCCCCGGGACACTGTGTTATCCA 300
QY 558 GATGGTCCAGAGGAGGAGGCTCGCTGTGCTGTGGGGTACTGTGCTCTACTCCAGCCT 617
DB 301 GATGGTCCAGAGGAGGAGGCTCGCTGTGCTGTGGGGTACTGTGCTCTACTCCAGCCT 360
QY 618 CATGGCGCTGCTGTGCTCTCGCCACCGTGTGTGCAACTCGGCGCATGGCACTCTTA 677
DB 361 CATGGCGCTGCTGTGCTCTCGCCACCGTGTGTGCAACTCGGCGCATGGCACTCTTA 420
QY 678 TCGCATGACACCGGCGGCTGTGACGCGGACCCGCGCTCTCTGACACGAGGACTGTGCCGAGCC 737
DB 421 TCGCATGACACCGGCGGCTGTGACGCGGACCCGCGCTCTCTGACACGAGGACTGTGCCGAGCC 480
QY 738 GGGCGCGGAGCGGAGGAGGAGCGTCCCTCAGCCCCCTGAGAGAGCTGATCACTCTGCT 797
DB 481 GGGCGCGGAGCGGAGGAGGAGCGTCCCTCAGCCCCCTGAGAGAGCTGATCACTCTGCT 540
QY 798 GCTGCGCTGATGACACCGTCTCTTCACTATGTGTCTCTGCGCCGTAATT 846
DB 541 GCTGCGCTGATGACACCGTCTCTTCACTATGTGTCTCTGCGCCGTAATT 589

RESULT 7
US-10-225-567A-286
/ Sequence 286, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenna C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A

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;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/257,144
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 2292
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 286
;; LENGTH: 495
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-225-567A-286

Query Match 40.4%; Score 436; DB 15; Length 495;
Best Local Similarity 100.0%; Pred. No. 2,3e-117;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GGTGTCACCTCGGCGCATGGCACTCTATGCGATGACCGGCGGTGAGCGGA 704
DB 1 GGTGTCACCTCGGCGCATGGCACTCTATGCGATGACCGGCGGTGAGCGGA 60
QY 705 CCGGCGCTCTGACACGAGGACTGTGCGAGCGCGCGGAGCGGAGGAAAGCGTCCC 764
DB 61 CCGGCGCTCTGACACGAGGACTGTGCGAGCGCGCGGAGCGGAGGAAAGCGTCCC 120
QY 765 TCAGCCCCCTGAGAGAGCTGATCCTCTGCTGCTGCGCTGATGACCGTCTTTCAC 824
DB 121 TCAGCCCCCTGAGAGAGCTGATCCTCTGCTGCTGCGCTGATGACCGTCTTTCAC 180
QY 825 TATGTTCTCTGCGCCGTAATTTATGCGCTTACTATGAGCATTTAAGGATGCAAGA 884
DB 181 TATGTTCTCTGCGCCGTAATTTATGCGCTTACTATGAGCATTTAAGGATGCAAGA 240
QY 885 GAAAAACAGAGCCTCTGAAGAGCAGAGACCTCCGAGCCTTGCGATTTCTATCTGTAT 944
DB 241 GAAAAACAGAGCCTCTGAAGAGCAGAGACCTCCGAGCCTTGCGATTTCTATCTGTAT 300
QY 945 TTCAATTGTGACCTTGTGATTTTATCATTTTCAATCTCCAGTATTTTCCGATATTTT 1004
DB 301 TTCAATTGTGACCTTGTGATTTTATCATTTTCAATCTCCAGTATTTTCCGATATTTT 360
QY 1005 TCACAAGATTTTCATTAAGCCTCTTATGATGACGAGCGGTGAGCAATTTCCACTAAT 1064
DB 361 TCACAAGATTTTCATTAAGCCTCTTATGATGACGAGCGGTGAGCAATTTCCACTAAT 420
QY 1065 GGAATCCAGTCTGTGA 1080
DB 421 GGAATCCAGTCTGTGA 436

RESULT 8

US-10-029-386-23781
; Sequence 23781, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Ranzel, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23781
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUE 7.00e-59
;; OTHER INFORMATION: NT HIT: U13332.1, EVALUE 0.00e+00
;; OTHER INFORMATION: EST_HUMAN HIT: A1460323.1, EVALUE 2.00e-16
US-10-029-386-23781

Query Match 34.4%; Score 371; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 2,5e-98;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 TTGCGCTTCTTATGATGCTTCTTTGGGCTCTCTGAGACATGCACTCCTGGCATGGA 381
DB 1 TTGCGCTTCTTATGATGCTTCTTTGGGCTCTCTGAGACATGCACTCCTGGCATGGA 60
QY 382 CTGAGATGCTGCTCTCCCTTACGAGGACCTTTCTTACGAGGACATGCACTCCTGGC 441
DB 61 CTGAGATGCTGCTCTCCCTTACGAGGACCTTTCTTACGAGGACATGCACTCCTGGC 120
QY 442 CTGGGCGCATGCTGAGCCCGGCTGTGAGCGCTTCTCTGCTTCTGCGGCTACT 501
DB 121 CTGGGCGCATGCTGAGCCCGGCTGTGAGCGCTTCTCTGCTTCTGCGGCTACT 180
QY 502 TTCAATGAGGCTTGGGAGGTTGCTGAGATGCTGCGCGGACCTGAGGCTTTATCCAGATG 561
DB 181 TTCAATGAGGCTTGGGAGGTTGCTGAGATGCTGCGCGGACCTGAGGCTTTATCCAGATG 240
QY 562 GTCCAGAGAGAGGCTGCTGTGCTGCTGAGGATCTGTGCTCTACTCAAGCCTGATG 621
DB 241 GTCCAGAGAGAGGCTGCTGTGCTGCTGAGGATCTGTGCTCTACTCAAGCCTGATG 300
QY 622 GCGCTGCTGCTCTGCGCACCGTCTGTGCAACTCTGCGGCAATGCGCAACTCTATGG 681
DB 301 GCGCTGCTGCTCTGCGCACCGTCTGTGCAACTCTGCGGCAATGCGCAACTCTATGG 360
QY 682 ATGCAACCGCG 692
DB 361 ATGCAACCGCG 371

RESULT 9

US-10-108-714-3
; Sequence 3, Application US/10108714
; Publication No. US20020128445A1
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: No. US20020128445A1 Human Prostaglandin EP Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/10/108,714
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157) ... (1233)
US-10-108-714-3

Query Match 20.4%; Score 220.6; DB 13; Length 2296;
Best Local Similarity 57.8%; Pred. No. 7,6e-54;
Matches 557; Conservative 0; Mismatches 349; Indels 57; Gaps 7;

QY 48 AGGCACTCGGGGGGATGGGGGGTGGCTTTACAGACCGGCTCTGGGCAACTGCT 107
DB 219 AGGCAAGCCAGCCACTGCTCCGTATGTTCTGCGCGGGGCTGGGCAACTCAT 278

PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/390,965
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US 60/392,480
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/394,128
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,783
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 60/403,221
PRIOR FILING DATE: 2002-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157)...(1233)
US-10-352-684A-35

Query Match 20.3%; Score 219; DB 17; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-53;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

48 AGGCAACTGGGCGGTATGGGCGGGGCTCTTACAGACCGGCTCTGCGCAACTGCT 107
|||
219 AGCGGAAGCCGACCATCAGCTCCGTCGATGTTCTCGCGGGGTGTGGGAACTCAT 278
108 GGCCTGAGGAGCTGCTGCGCGCTCGGGCTGGGGT--GGTCTGCGGCGCTCCACTGCG 165
279 AGACATGGGCTGCTGCTGCGCGCTCGGGGAGAGCTGGGGTGCAGCCCGCGCAG 338
166 CCGCTGCC-CTCGGTCTTACATGCTGTGTGTGCTGACGCTGACCGACTTGTGG 224
339 GAGCTCCCTCTCTTGTCCAGCTGCTGAGACCGAGCTGTTCACGACCTGCTCG 398
225 CAAGTCCCTCTTAAGCCCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 284
399 GACCTCCCTCATAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
285 GCTTGGCGCGCATGGAACAATGTTGTGCAAGCTTGTGCTTCTTCTTCTTCTT 344
459 ACTGGGCGCC-----GAGAGCGCGGCTGCACTTCTTCTTCTTCTTCTTCTT 512
345 TGGGCTCTCTGACACTGCACTCTGCGCATGAGCACTGAGTGTGCTTCTCTAGG 404
513 CAGCTGCGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
405 GCACTCTTCTTACAGAGGCAATCACTGCGCTGCGCTGCGCTGCTGCTGCTGCT 464
573 GCACTCTTCTTACAGAGGCGCGCTGCTGCGCTGCGCTGCGCTGCTGCTGCTG 632
465 GGTAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524
633 CATCTATGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
525 GAGTATCTGCGCGGCACTGCTGCTTATTCAGATGCTCAGAGAGGCTGCTGCT 584
693 CAGTATCTGCGCGGCACTGCTGCTTATTCAGATGCTCAGAGAGGCTGCTGCT 734
585 GGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644
735 ---GACCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791
645 GGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
792 CCGCTGCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 851
703 CACCCGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762

DB 852 CCGCTGCGGACTTCTCTGCGAGTGCGCGGCGCGCGCGCGCGCGCGCGCGGGA 911
QY CTCAGCCCTCT---GAGAGAGCTGATCACTCTGCTGCTGCTGCTGCTGCTGCT 818
DB 912 AAGGTGTCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
QY CTTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878
DB 972 CTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
QY 879 CAG 938
DB 1012 -ATGAATGAAACCTCTTCCGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
QY 939 TGTGATTTCAATTTGAGACCTTGAATTTTATCATTTTCAGATCTCCAGATTTGGAT 998
DB 1071 AATTAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1130
QY 999 ATT 1001
DB 1131 AAT 1133

RESULT 13
US-10-366-288-35
Sequence 35, Application us/10366288
Publication No. US20030216288A1

GENERAL INFORMATION:
APPLICANT: Powell, Douglas
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING
TITLE OF INVENTION: 34021, 1720, 1683, 1557, 1682, 1675, 12825, 9952, 5816,
TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
FILE REFERENCE: MP102-025P1R0NMNIM
CURRENT APPLICATION NUMBER: US/10/366,288
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 60/357,391
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380,249
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/391,306
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/406,297
PRIOR FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/412,007
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: 60/417,508
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/432,318
PRIOR FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo Sapien
US-10-366-288-35

Query Match 20.3%; Score 219; DB 17; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-53;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

48 AGGCAACTGGGCGGTATGGGCGGGGCTCTTACAGACCGGCTCTGCGCAACTGCT 107
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219 AGCGGAAGCCGACCATCAGCTCCGTCGATGTTCTGCGCGGGGTGTGGGAACTCAT 278
108 GGCCTGAGGAGCTGCTGCGCGCTCGGGCTGGGGT--GGTCTGCGGCGCTCCACTGCG 165
279 AGACATGGGCTGCTGCTGCGCGCTCGGGGAGAGCTGGGGTGCAGCCCGCGCAG 338
166 CCGCTGCC-CTCGGTCTTACATGCTGTGTGTGCTGACGCTGACCGACTTGTGG 224


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OY      939  TGTGATTCATTGTGAGACCCCTTGATTTTATTCATTTTCAGATCCAGTATTCGGAT 998
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Db      1071  AATTAAATTCATTAATTCAGACCTTGAGGTCTTTCGCATCCTTAGGCTCTGTCTGAGACT 1130
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OY      999  ATT 1001
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Db      1131  AAT 1133

RESULT 15
US-10-755-889-91
; Sequence 91, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-755-889-91

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:00:43 ; Search time 21.3756 Seconds
(without alignments)
1253.721 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFYRCQNTSVKGNLSA.....IRPLRYRCSNSTNMESL 359

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUTS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1864	100.0	359	2 US-08-812-203-3	Sequence 3, Appli
2	1864	100.0	359	3 US-09-300-864-3	Sequence 3, Appli
3	1864	100.0	359	3 US-09-598-418-3	Sequence 3, Appli
4	688	36.9	358	1 US-08-239-431A-4	Sequence 4, Appli
5	688	36.9	358	1 US-08-257-423-4	Sequence 4, Appli
6	683	36.6	358	4 US-03-826-509-559	Sequence 559, App
7	667	35.8	358	2 US-08-463-081B-6	Sequence 6, Appli
8	667	35.8	358	2 US-08-461-379A-6	Sequence 6, Appli
9	667	35.8	358	2 US-08-462-390B-6	Sequence 6, Appli
10	667	35.8	358	3 US-08-463-074B-6	Sequence 6, Appli
11	667	35.8	358	3 US-08-465-585C-6	Sequence 6, Appli
12	667	35.8	358	3 US-08-652-446-6	Sequence 6, Appli
13	597	32.0	386	1 US-08-134-012-3	Sequence 3, Appli
14	597	32.0	386	1 US-08-520-519-3	Sequence 3, Appli
15	597	32.0	386	1 US-09-039-798-3	Sequence 3, Appli
16	458.5	24.6	513	1 US-08-390-162-6	Sequence 6, Appli
17	458.5	24.6	513	1 US-08-685-945B-6	Sequence 6, Appli
18	443	23.8	488	1 US-08-115-365-2	Sequence 2, Appli
19	443	23.8	488	1 US-08-586-897-2	Sequence 2, Appli
20	440	23.6	488	4 US-09-826-509-561	Sequence 561, App
21	308	16.5	365	1 US-08-390-162-2	Sequence 2, Appli
22	308	16.5	365	1 US-08-685-945B-2	Sequence 2, Appli
23	307.5	16.5	361	1 US-08-390-162-4	Sequence 4, Appli
24	307.5	16.5	361	1 US-08-685-945B-4	Sequence 4, Appli
25	302	16.2	385	1 US-08-416-756A-3	Sequence 3, Appli
26	302	16.2	385	4 US-08-880-865-3	Sequence 3, Appli
27	297.5	16.0	390	3 US-08-155-005A-4	Sequence 4, Appli

28	297.5	16.0	390	3 US-08-155-005A-17	Sequence 17, Appli
29	297.5	16.0	390	3 US-09-363-783-4	Sequence 4, Appli
30	297.5	16.0	390	3 US-09-363-783-17	Sequence 17, Appli
31	297.5	16.0	390	4 US-09-661-758A-4	Sequence 4, Appli
32	297.5	16.0	390	4 US-09-661-758A-17	Sequence 17, Appli
33	294	15.8	388	3 US-08-155-005A-6	Sequence 6, Appli
34	294	15.8	388	3 US-09-363-783-6	Sequence 6, Appli
35	294	15.8	388	4 US-09-661-758A-6	Sequence 6, Appli
36	293.5	15.7	365	3 US-08-155-005A-8	Sequence 8, Appli
37	293.5	15.7	365	3 US-09-363-783-8	Sequence 8, Appli
38	293.5	15.7	365	4 US-09-661-758A-8	Sequence 8, Appli
39	289.5	15.5	343	4 US-09-054-272-6	Sequence 6, Appli
40	267	14.3	378	4 US-08-416-756A-4	Sequence 4, Appli
41	267	14.3	378	4 US-08-880-865-4	Sequence 4, Appli
42	255.5	13.7	402	2 US-08-068-729-4	Sequence 4, Appli
43	255.5	13.7	402	3 US-09-255-671-4	Sequence 4, Appli
44	255.5	13.7	402	4 US-09-395-366-4	Sequence 4, Appli
45	252.5	13.5	402	4 US-09-826-509-557	Sequence 557, App

ALIGNMENTS

RESULT 1
US-08-812-203-3
Sequence 3, Application US/08812203
Patent No. 5958723
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: BOIE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,203
FILING DATE: 06-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-203-3
Query Match 100.0%; Score 1864; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 16-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MKSPFYRCQNTTSVEKGNASVMGCVLFSTGLGNLALGLIASSGLGWCRRRLRPLPSV 60
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKSPFYRCQNTTSVEKGNASVMGCVLFSTGLGNLALGLIASSGLGWCRRRLRPLPSV 60
QY 61 FYMLVCGLTITDILGKCLSPVLAAYAOQRSRLVLAAPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTITDILGKCLSPVLAAYAOQRSRLVLAAPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLAMALECWLISLGHFFPYRRHITTLRLGALVAPVSAFSLAFCAIPMGFGKRVQYCPG 180
DB 121 LQLLAMALECWLISLGHFFPYRRHITTLRLGALVAPVSAFSLAFCAIPMGFGKRVQYCPG 180
QY 181 TWCFIQWHEGSLSVGYSLVYSSLMALLVATVLCNIGAMRNLYAMHRRLORHPRSC 240
DB 181 TWCFIQWHEGSLSVGYSLVYSSLMALLVATVLCNIGAMRNLYAMHRRLORHPRSC 240
QY 241 RDCAEPRADGRASPOPLEELDHLLALMTVLFMCSLPVYRAYYGAFDYVEKNRTS 300
DB 241 RDCAEPRADGRASPOPLEELDHLLALMTVLFMCSLPVYRAYYGAFDYVEKNRTS 300
QY 301 EEAEDLRALRFLSVISIVDPWIFIFRSPVFRIFPHKIFIRPLRYRSCNSTMESSL 359
DB 301 EEAEDLRALRFLSVISIVDPWIFIFRSPVFRIFPHKIFIRPLRYRSCNSTMESSL 359

RESULT 2
US-09-300-864-3
Sequence 3, Application US/09300864
Patent No. 6214972
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
BOLE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,864
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-864-3

Query Match 100.0%; Score 1864; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGNASVMGCVLFSTGLGNLALGLIASSGLGWCRRRLRPLPSV 60
DB 1 MKSPFYRCQNTTSVEKGNASVMGCVLFSTGLGNLALGLIASSGLGWCRRRLRPLPSV 60
QY 61 FYMLVCGLTITDILGKCLSPVLAAYAOQRSRLVLAAPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTITDILGKCLSPVLAAYAOQRSRLVLAAPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLAMALECWLISLGHFFPYRRHITTLRLGALVAPVSAFSLAFCAIPMGFGKRVQYCPG 180
DB 121 LQLLAMALECWLISLGHFFPYRRHITTLRLGALVAPVSAFSLAFCAIPMGFGKRVQYCPG 180
QY 181 TWCFIQWHEGSLSVGYSLVYSSLMALLVATVLCNIGAMRNLYAMHRRLORHPRSC 240
DB 181 TWCFIQWHEGSLSVGYSLVYSSLMALLVATVLCNIGAMRNLYAMHRRLORHPRSC 240
QY 241 RDCAEPRADGRASPOPLEELDHLLALMTVLFMCSLPVYRAYYGAFDYVEKNRTS 300
DB 241 RDCAEPRADGRASPOPLEELDHLLALMTVLFMCSLPVYRAYYGAFDYVEKNRTS 300
QY 301 EEAEDLRALRFLSVISIVDPWIFIFRSPVFRIFPHKIFIRPLRYRSCNSTMESSL 359
DB 301 EEAEDLRALRFLSVISIVDPWIFIFRSPVFRIFPHKIFIRPLRYRSCNSTMESSL 359

RESULT 3
US-09-598-418-3
Sequence 3, Application US/09598418
Patent No. 6395499
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
BOLE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,418
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-598-418-3

Query Match 100.0%; Score 1864; DB 3; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1e-166;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFRRCQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 60
 DB 1 MKSPFRRCQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 60
 QY 61 FYMLVCGITVTYDILGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 120
 DB 61 FYMLVCGITVTYDILGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 120
 QY 121 LQILAMLECLSLGHPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 180
 DB 121 LQILAMLECLSLGHPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 180
 QY 181 TWCFIQVHEEGSLSVLGYSVLSSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCT 240
 DB 181 TWCFIQVHEEGSLSVLGYSVLSSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCT 240
 QY 241 RDCAEPRADGRASPOPLEEIDHLLALMTVLFMGSLPIYIYAYGAFDYKERTS 300
 DB 241 RDCAEPRADGRASPOPLEEIDHLLALMTVLFMGSLPIYIYAYGAFDYKERTS 300
 QY 301 EEAEDLALRPLSVISYVDPWIFPIFRSPVPRIFPKIFIRPLRYRSRCSNSTMESL 359
 DB 301 EEAEDLALRPLSVISYVDPWIFPIFRSPVPRIFPKIFIRPLRYRSRCSNSTMESL 359

RESULT 4

US-08-239-431A-4
 ; Sequence 4, Application US/08239431A
 ; Patent No. 5716835

GENERAL INFORMATION:
 APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: NOVEL HUMAN EP PROTAGLANDIN RECEPTOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/239,431A
 FILING DATE: 05-MAY-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelien, Ned A
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: ALRGN.053A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-239-431A-4

Query Match 36.9%; Score 688; DB 1; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.9e-56;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 CQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 65
 DB 13 CQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 65
 QY 66 CGITVTYDILGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 125
 DB 72 TELVFTDLGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 125
 QY 126 MALECMWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 185
 DB 130 MALECMWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 185
 QY 186 QVHEEGSLSVLGYSVLSSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCT 245
 DB 190 R-HGR-----TVLQVLAIVLCNLGAMRNLVAMHRLQHRPSCT 240
 QY 246 ----PRADGRASPOPLEEIDHLLALMTVLFMGSLPIYIYAYGAFDYKERTS 301
 DB 241 GRCGPGARRRGERVSMEEIDHLLALMTVLFMGSLPIYIYAYGAFDYKERTS 291
 QY 302 EAE--DLRALRPLSVISYVDPWIFPIFRSPVPRIFPKIFIRPLRYRSRCSNSTMES 357
 DB 292 RKEKMDLALRPLSVISYVDPWIFPIFRSPVPRIFPKIFIRPLRYRSRCSNSTMES 350

RESULT 5

US-09-267-423-4
 ; Sequence 4, Application US/09267423
 ; Patent No. 6395878

GENERAL INFORMATION:
 APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: No. 6395878 Human Prostaglandin EP Receptor
 FILE REFERENCE: 17023 DIV CIP
 CURRENT APPLICATION NUMBER: US/09/267,423
 CURRENT FILING DATE: 1999-03-12
 EARLIER APPLICATION NUMBER: 09/019,393
 EARLIER FILING DATE: 1998-02-05
 EARLIER APPLICATION NUMBER: 08/239,431
 EARLIER FILING DATE: 1994-05-05
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-267-423-4

Query Match 36.9%; Score 688; DB 3; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.9e-56;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 CQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 65
 DB 13 CQNTTSVEKGNASVAVGGVLFSTGLGNLALGLARSGLCGSRRLPLRPLPSV 65
 QY 66 CGITVTYDILGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 125
 DB 72 TELVFTDLGKCLISPVLAAYQNSLRVLAAPALNSLCQAFAFMSPFGLSST 125
 QY 126 MALECMWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 185
 DB 130 MALECMWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCALPFGKGFVQYCPG 185

Db 130 MALERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSLPILDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSSMLLVATVLCNIGANBNLYAMHRIQHRHRSCTRCAE 245
Db 190 R--HGR-----TALQYATLTLTLIVSLACNFSVLNIRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLALMTITFAVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNNTNES 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAILRPVILMRSVLCRISLRTQDATQTSCTOS 350

RESULT 6
US-09-826-509-559
; Sequence 559, Application US/09026509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brinnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826, 509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO: 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-559

Query Match 36.6%; Score 683; DB 4; Length 358;
Best Local Similarity 43.5%; Pred. No. 5.7e-56;
Matches 156; Conservative 54; Mismatches 119; Indels 30; Gaps 10;
QY 8 CQNTSVKGNNAVMGVLFSTGLGNLALGLIARSLG--WCSRRLRPLRPVPMV 65
Db 13 CETRQMPPESSPAISSVMFSAGVGNLIALALARRRGVGSAGRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLSPVLAAYANRSIRVLAAPALDNLCOAFAPFMSFPGSLSTLQILA 125
Db 72 TELVFTDLGCLISPVLAAYANRSIRVLAAPALDNLCOAFAPFMSFPGSLSTLQILA 129
QY 126 MALECWLSLGHPEFYRRHITRLGALVAPVVSASFALFCAFPWGFQKFOYCGTWCFI 185
Db 130 MALEERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSLPILDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSSMLLVATVLCNIGANBNLYAMHRIQHRHRSCTRCAE 245
Db 190 R--HGR-----TALQYATLTLTLIVSLACNFSVLNIRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLALMTITFAVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNNTNES 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAILRPVILMRSVLCRISLRTQDATQTSCTOS 350

RESULT 7
US-08-463-081B-6
; Sequence 6, Application US/08463081B

; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadell, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide.
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463, 081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-081B-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;
QY 8 CQNTSVKGNNAVMGVLFSTGLGNLALGLIARSLG--WCSRRLRPLRPVPMV 65
Db 13 CETRQMPPESSPAISSVMFSAGVGNLIALALARRRGVGSAGRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLSPVLAAYANRSIRVLAAPALDNLCOAFAPFMSFPGSLSTLQILA 125
Db 72 TELVFTDLGCLISPVLAAYANRSIRVLAAPALDNLCOAFAPFMSFPGSLSTLQILA 129
QY 126 MALECWLSLGHPEFYRRHITRLGALVAPVVSASFALFCAFPWGFQKFOYCGTWCFI 185
Db 130 MALEERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSLPILDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSSMLLVATVLCNIGANBNLYAMHRIQHRHRSCTRCAE 245
Db 190 R--HGR-----TALQYATLTLTLIVSLACNFSVLNIRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLALMTITFAVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNNTNES 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAILRPVILMRSVLCRISLRTQDATQTSCTOS 350

RESULT 8
US-08-461-379A-6
Sequence 6, Application US/08461379A
Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
VECTOR OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US88 08/330,108; 08/104,736
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-379A-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAAMGVLPSTGLGNLALGLIARSLG--WCSRRPLRLPSPVFMV 65
DB 13 CETRQWPPPEBPSPAISSVMSAGVLGNLIELALARRWQGDVGSAGRRSSL-SLFVVLV 71
QY 66 CGLTVDLGLCKLSPVLAAYVQNSRLVLAAPALDNLCOAFAPFMSFGSLSTLQLLA 125
DB 72 TELVFTDLGTCLISPVLAAYVQNSRLVLAAPALDNLCOAFAPFMSFGSLSTLQLLA 125
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVSAFSLAFCAFPFGKFPVQYCGTWCPI 185
DB 130 MALEERYLSIGHPPFYRRHITRLGALVAPVSAFSLAFCAFPFGKFPVQYCGTWCPI 185
QY 186 QMVEHESLSLVGVSYSLSMLLVATVLCNGAMRNLYAMHRLQHRPSTRCDAE 245
DB 190 R--HGR-----TAYLQIYATLLILLIVSLACNFSVLTNIRHRRSR--SRGSPSLGS 240
QY 246 ----PRADGEASPOPLEEDHLLALMTVLFTMCSLPVYRAYGAFDVEKENTSE 301
DB 241 GGGPGARRRGERGVSMAEEDHLLALMTVLFTMCSLPVYRAYGAFDVEKENTSE 301
QY 302 EAE--DLRALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR-PLRYRSRCSNSTNMS 357
DB 292 RKEKMDLQALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR-PLRYRSRCSNSTNMS 357

RESULT 9
US-08-462-390B-6
Sequence 6, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US88 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US88 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: US88 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-390B-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAAMGVLPSTGLGNLALGLIARSLG--WCSRRPLRLPSPVFMV 65
DB 13 CETRQWPPPEBPSPAISSVMSAGVLGNLIELALARRWQGDVGSAGRRSSL-SLFVVLV 71
QY 66 CGLTVDLGLCKLSPVLAAYVQNSRLVLAAPALDNLCOAFAPFMSFGSLSTLQLLA 125
DB 72 TELVFTDLGTCLISPVLAAYVQNSRLVLAAPALDNLCOAFAPFMSFGSLSTLQLLA 125
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVSAFSLAFCAFPFGKFPVQYCGTWCPI 185
DB 130 MALEERYLSIGHPPFYRRHITRLGALVAPVSAFSLAFCAFPFGKFPVQYCGTWCPI 185
QY 186 QMVEHESLSLVGVSYSLSMLLVATVLCNGAMRNLYAMHRLQHRPSTRCDAE 245
DB 190 R--HGR-----TAYLQIYATLLILLIVSLACNFSVLTNIRHRRSR--SRGSPSLGS 240
QY 246 ----PRADGEASPOPLEEDHLLALMTVLFTMCSLPVYRAYGAFDVEKENTSE 301
DB 241 GGGPGARRRGERGVSMAEEDHLLALMTVLFTMCSLPVYRAYGAFDVEKENTSE 301
QY 302 EAE--DLRALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR-PLRYRSRCSNSTNMS 357
DB 292 RKEKMDLQALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR-PLRYRSRCSNSTNMS 357

Db 292 RKERMDLQALRFLSINSIIDPWVFAILRPVLRIMRSVLCGRISLRQTQATQTSCTOS 350

RESULT 10

US-08-463-074B-6

Sequence 6, Application US/08463074B

Patent No. 6020155

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol

TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI

(B) STREET:

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,074B

FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/104,736

FILING DATE: 10-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,066

FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-463-074B-6

Query Match 35.8%; Score 667; DB 3; Length 358;

Best Local Similarity 42.9%; Pred. No. 1.8e-54;

Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

Db 8 CQNTTSVEKNSAVMGVLPSTGLGNLALGLIARSGLG--WCSRRPLRPDSVFMV 65

Db 13 CTRQWPPPPSPAISSVMSAGVGLNLIETALARRWQGVCSAGRSSL-SLFHVLV 71

Db 66 CGLVTDLIGKCLISPVLAAYANRSLRVAPALDNLSCQAFPMFSGLSSTQLOLA 125

Db 72 TELVFTDLIGCLISPVLAAYANRSLRVAPALDNLSCQAFPMFSGLSSTQLOLA 129

Db 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCALPFMGFGKPVQYCPGTWCFI 185

Db 130 MALERYLSIGHPIFYQRRVRSGLAVLPVIVAVSLFCSLPILDYQYQYVCGTWCFFI 189

Db 186 QMHEBSLSVLGVSIVSYSLMALVLAIVLCNIGAMRNLYAMHRLQHRPSCSTRCAE 245

Db 190 R--HGR-----TAYLQIYATILLLIIVSVLACNFSVILNIRHRRSR--SRGSPSLGS 240

Db 246 ----PRADGREALPQPLEEDHLLALMTVLFTMCSLPVIRAYYGAFAVDKEXKNTSE 301

Db 241 GGGPGARRRGERVSMABETDHLILALMTITTFVAVCSLPPTIFAY-----METS 291

Db 302 EAE--DRLALRFLSVISIVDPWIFIRFSPVRIFFHKIFIR-DLRYRSRCSNSTNMS 357

Db 292 RKERMDLQALRFLSINSIIDPWVFAILRPVLRIMRSVLCGRISLRQTQATQTSCTOS 350

RESULT 11

US-08-465-585C-6

Sequence 6, Application US/08465585C

Patent No. 6027914

GENERAL INFORMATION:

APPLICANT: Smith, K. A., & Beadling, C.

TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI

(B) STREET:

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,585C

FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/330,108

FILING DATE: 27-OCT-1994

APPLICATION NUMBER: USN 08/104,736

FILING DATE: 10-AUG-1993

APPLICATION NUMBER: USN 07/796,066

FILING DATE: 20-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 4894210

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-585C-6

Query Match 35.8%; Score 667; DB 3; Length 358;

Best Local Similarity 42.9%; Pred. No. 1.8e-54;

Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

Db 8 CQNTTSVEKNSAVMGVLPSTGLGNLALGLIARSGLG--WCSRRPLRPDSVFMV 65

Db 13 CTRQWPPPPSPAISSVMSAGVGLNLIETALARRWQGVCSAGRSSL-SLFHVLV 71

Db 66 CGLVTDLIGKCLISPVLAAYANRSLRVAPALDNLSCQAFPMFSGLSSTQLOLA 125

Db 72 TELVFTDLIGCLISPVLAAYANRSLRVAPALDNLSCQAFPMFSGLSSTQLOLA 129

Db 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCALPFMGFGKPVQYCPGTWCFI 185

Db 130 MALERYLSIGHPIFYQRRVRSGLAVLPVIVAVSLFCSLPILDYQYQYVCGTWCFFI 189

Db 186 QMHEBSLSVLGVSIVSYSLMALVLAIVLCNIGAMRNLYAMHRLQHRPSCSTRCAE 245

Db 190 R--HGR-----TAYLQIYATILLLIIVSVLACNFSVILNIRHRRSR--SRGSPSLGS 240

Db 246 ----PRADGREALPQPLEEDHLLALMTVLFTMCSLPVIRAYYGAFAVDKEXKNTSE 301

Db 241 GGGPGARRRGERVSMABETDHLILALMTITTFVAVCSLPPTIFAY-----METS 291

QY 302 EAE--DIRALRFLSVISIVDPWFIFIRSPVFRIFPKIKIR-PLRYRSCSNSTNMES 357
Db 292 RKEMDQLARFLSINSIIDPWVAILRPVLRMLRSVLCRISLRTOADTQTSCTOS 350

RESULT 12

US-08-652-446-6
Sequence 6, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles (B) STREET:
STATE: California 444 South Flower St. - Suite 1900
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,350
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vytiana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-652-446-6

Query Match 35.8%; Score 667; DB 3; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CONTTSVEKGNSSAMGCVLFTSLGNLALGLARSGLG--WCSRRPLRLPSVFMV 65
Db 13 CETRQWPPSPESPAISSVMFSAGVLTGLIALALARRQODVGCASARRSSL-SLFHVLV 71
QY 66 CGLTVTDLGGKCLISPVLAAYQNSRLVAPALDNLCOAFAPFMSFFGLSTQLLA 125
Db 72 TELVFTDLGTCILSPVLASVARNQVLALP--ESRASTYAFAMTFSLATMLMLFT 129
QY 126 MALEWLSLGHPPFFRRHITLRIGALVAPVVSASFALCFLPMGPKFYQYCGTWCFI 185
Db 130 MALERYLSIGHPPFYORVRSGLAVLPVIYVVSILFCSLPILDQYQYQYCGTWCFI 189
QY 186 QMHEEGSLSLGVSYSLSMALVLTATVLCNIGAMRNLYAMHRLQRPSCCTRDCAE 245
Db 190 R--HGR-----TAYLQIYATLLILIVSVLACFSVILNIRHRRRR--SRGSPSLG 240
QY 246 ----PRADGEASPPLELDHLLILMTVLTMSCLPVYRAYYGAFDVAEKNTSE 301
Db 241 GGGPGARRRGERVSMAEETDHLILALMTITFAVCSLPITIRAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWFIFIRSPVFRIFPKIKIR-PLRYRSCSNSTNMES 357
Db 292 RKEMDQLARFLSINSIIDPWVAILRPVLRMLRSVLCRISLRTOADTQTSCTOS 350

RESULT 13

US-08-134-012-3
Sequence 3, Application US/08134012
Patent No. 5516652
GENERAL INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Bole, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipeitz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Wallen
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

LENGTH: 386 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-039-798-3

Query Match 32.0%; Score 597; DB 3; Length 386;
 Best local Similarity 42.3%; Pred. No. 7,2e-48;
 Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;

QY	8	CONTTSYEKNSAVMGVLFSTGLGNLALGLIARSGLGWCSRRLPLPSVFYMLVCG	67
DB	5	CRNLTIVRGSGVPATSTLMFVAGVGNGLGILS-----ARRPAR--PSAFVAVLTG	55
QY	68	LTVTDLGKCLLSPVLAAYANRSLAVLA---PALDNLCOAFAPFMSFPGLSSTIQL	124
DB	56	LAATDLGTSFLSPAVFVAAYARNSSLGLARGGPA---LCDAPAFAMTFEGLASMLILF	111
QY	125	AMALECWLSIGHPPFYRRHITLRLGALVAPVSAFSLAFCALPVMGFGKFVQYCPGTWCF	184
DB	112	AMAVERTLASHRYLYAQLDGRRCARLALPAIYAFCVLPCLPLGLIGOHQYCPGSMCF	171
QY	185	IQN--VHEEGLSVLGYSVLVSSIMALLVATVLCNLGAMENLYAMRRLORHPRSCCTRD	242
DB	172	LRRMWAQPGGA---AFSLAYAGLVALLVAIFLCNGSVTLSLCRMVYRQQRHQS----	223
QY	243	CAEPRADGRASPOPL---EELDHLLALMTVLFTWCSPVIYRAYGAFKDYKEKRT	299
DB	224	-----LQPRPRGTGEVDHLILALMTVMVAVCSLPLTIRCTQAVAP-----DS	268
QY	300	SEEAEDRALRPLSVISIVDPWIFLIRSPVER	332
DB	269	SSEMGLLAFRYAFNPILDPWVFLPRKAVFQ	301

Search completed: April 22, 2005, 21:30:47
 Job time: 21.3756 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 17:53:08 ; Search time 65.771 Seconds
(without alignments)
2111.067 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFVRCQNTTSVEKNGSA.....IRPLRYRSCNSTNMESL 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1864	100.0	359	2	AAW03516 Prostagla
2	1864	100.0	359	4	AAW79009 Human pro
3	1864	100.0	359	6	ABP81901 Human pro
4	1864	100.0	359	7	ADDA48182 Human pro
5	1864	100.0	359	8	ADO29614 Human GPC
6	1864	100.0	359	4	ABBI2000 Human pro
7	1864	100.0	359	4	AAW79993 Human pro
8	1864	100.0	359	7	ADDE09040 Novel pro
9	1757.5	94.3	424	7	ADDE07993 Novel pro
10	1580	84.8	369	3	AAV94346 Human cel
11	1386.5	74.4	357	7	ADDA48180 Rat Prote
12	1347.5	72.3	357	8	ADO29615 Mouse GPC
13	1346.5	72.2	357	2	AAW84708 Prostagla
14	752	40.3	144	8	ADP551749 Human PRO
15	707.5	38.0	362	8	ADO29619 Mouse GPC
16	689	37.0	358	6	ABP81903 Human pro
17	689	37.0	358	7	ADDE04057 Human pro
18	689	37.0	358	7	ADK32578 Hematology
19	689	37.0	358	8	ADO29618 Human GPC
20	689	37.0	358	8	ADRI4091 Human NF-
21	689	37.0	358	8	ADRA43385 Prostagla
22	689	37.0	609	2	AAV41279 Fusion pr
23	688	36.9	358	2	AAW44246 Human HP4
24	688	36.9	358	5	ABG30499 Human HP4
25	688	36.9	358	8	ADO05738 Human pro

26	683	36.6	358	4	ABBS56383	Abb56383 Non-endog
27	667	35.8	358	2	AAW08135	Aaw08135 Human cyt
28	667	35.8	358	3	AAW87954	Aay87954 Human CR3
29	597	32.0	386	2	AAAR1979	Aar81979 Human pro
30	597	32.0	386	2	AAAR1980	Aar81980 Human pro
31	597	32.0	386	6	ABP81900	Abp81900 Human pro
32	597	32.0	386	7	ADP03580	Adp03580 Human GPC
33	597	32.0	386	8	ADO29626	Ado29626 Human GPC
34	597	32.0	386	8	ADO95940	Ado95940 T cell ac
35	596.5	32.0	415	8	ADO29627	Ado29627 Mouse GPC
36	592	31.8	386	2	AAAR74915	Aar74915 Prostagla
37	585.5	31.4	416	2	AAAR1981	Aar81981 Rat proet
38	519.5	27.9	256	8	ADQ95984	Adq95984 T cell ac
39	518.5	27.8	284	8	ADQ95982	Adq95982 T cell ac
40	518.5	27.8	289	7	ADMO5222	Adm05222 Human pro
41	516	27.7	253	8	ADP29755	Adp29755 Human sec
42	458.5	24.6	513	2	AAAR42282	Aar42282 PG22 rece
43	458.5	24.6	513	8	ADO29623	Ado29623 Mouse GPC
44	443	23.8	480	8	ADAR46683	Adar46683 Cancer-as
45	443	23.8	488	2	AAW02271	Aaw02271 Human pro

ALIGNMENTS

RESULT 1
AAW03516
ID AAW03516 standard; protein; 359 AA.
XX
AC AAW03516;
XX
DT 11-MAR-1997 (first entry)
XX
DE Prostaglandin DP receptor.
XX
KW Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;
KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
KW mouse; prostaglandin-related disease; therapy.
XX
OS Homo sapiens.
XX
PN WO9623066-A2.
XX
PD 01-AUG-1996.
XX
PF 23-JAN-1996; 96WO-CA000047.
XX
PR 26-JAN-1995; 95US-00378682.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;
XX
DR WPI; 1996-362690/36.
XX
DR N-PSDB; AAT37402.
XX
PT Human prostaglandin DP receptor and related DNA - used to identify
PS receptor modulators to treat prostaglandin-related diseases.
XX
XX Claim 2; Page 41; 49pp; English.

This sequence represents the human prostaglandin DP receptor. The DP receptor is the least ubiquitous and least abundant of the prostanoid receptors. The DP receptors are thought to be distributed mainly in blood platelets, smooth muscle of various tissues, and nervous tissue (including the central nervous system). However, many of the actions and distribution of the DP receptor is species dependent. This receptor is a G protein-coupled receptor which can specifically bind prostaglandin molecules. The DNA encoding this sequence was isolated using primers (see AAT37403 and AAT37404) based on the N-terminal sequence, and an internal sequence from purified mouse DP. The human prostaglandin DP receptor can be used to identify modulators of the receptor. The identified modulators can then be used to treat prostaglandin-related diseases, and for

CC modulating the effects of prostaglandins on the DP receptor
XX Sequence 359 AA;
SQ

Query Match 100.0%; Score 1864; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFFRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
DB 1 MKSPFFRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
QY 61 FYMLVGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLMALECWLSLGHFFYRRHITLRIGALVAPVVSFAFLAPCALPFGMGFGKVFQYCPG 180
DB 121 LQLLMALECWLSLGHFFYRRHITLRIGALVAPVVSFAFLAPCALPFGMGFGKVFQYCPG 180
QY 181 TWCFIQWHEBEGSLVGLSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHPRSCT 240
DB 181 TWCFIQWHEBEGSLVGLSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHPRSCT 240
QY 241 RDCAEPADGREGASPOPLELDHLLALMTVLTWCSLPVIYRAYYGAFKDVKEKNRTS 300
DB 241 RDCAEPADGREGASPOPLELDHLLALMTVLTWCSLPVIYRAYYGAFKDVKEKNRTS 300
QY 301 EEAEEDLRALRFLSVISIDVPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359
DB 301 EEAEEDLRALRFLSVISIDVPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359

RESULT 2
AAAM79009
ID AAAM79009 standard; protein; 359 AA.
XX
AC AAAM79009;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1671.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PR 20-JUN-2000; 2000US-00598075.
XX
PR 19-JUL-2000; 2000US-00620325.
XX
PR 01-SEP-2000; 2000US-00654936.
XX
PR 15-SEP-2000; 2000US-00663561.
XX
PR 20-OCT-2000; 2000US-00693325.
XX
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
XX
DR N-PSDB; AAK52142.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 4016-4017; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1864; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFFRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
DB 1 MKSPFFRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
QY 61 FYMLVGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLMALECWLSLGHFFYRRHITLRIGALVAPVVSFAFLAPCALPFGMGFGKVFQYCPG 180
DB 121 LQLLMALECWLSLGHFFYRRHITLRIGALVAPVVSFAFLAPCALPFGMGFGKVFQYCPG 180
QY 181 TWCFIQWHEBEGSLVGLSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHPRSCT 240
DB 181 TWCFIQWHEBEGSLVGLSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHPRSCT 240
QY 241 RDCAEPADGREGASPOPLELDHLLALMTVLTWCSLPVIYRAYYGAFKDVKEKNRTS 300
DB 241 RDCAEPADGREGASPOPLELDHLLALMTVLTWCSLPVIYRAYYGAFKDVKEKNRTS 300
QY 301 EEAEEDLRALRFLSVISIDVPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359
DB 301 EEAEEDLRALRFLSVISIDVPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359

RESULT 3
ABP81901
ID ABP81901 standard; protein; 359 AA.
XX
AC ABP81901;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human prostaglandin D2 receptor protein SEQ ID NO:287.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX

OS Homo sapiens.
XX WO200261087-A2.
XX PD 08-AUG-2002.
XX PF 19-DEC-2001; 2001WO-US050107.
XX PR 19-DEC-2000; 2000US-0257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burmer GC, Roush CL, Brown JP;
XX N-PSDB; ABZ42748.
XX WPI; 2003-046718/04.
XX DR N-PSDB; ABZ42748.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
XX Disclosure; Fig 1; 523pp; English.
XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
XX SQ Sequence 359 AA;
Query Match 100.0%; Score 1864; DB 6; Length 359;
Best Local Similarity 100.0%; Pred No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPFYRCQNTTSVEKNGSAVMGGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
DB 1 MKSPFYRCQNTTSVEKNGSAVMGGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
QY 61 FYMLVGLTVDLLGKLLSPVLLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120
DB 61 FYMLVGLTVDLLGKLLSPVLLAAYQNRSLRVLPALDNLSCQAFPMFSGLSST 120
QY 121 LQLLMALECWLSLGHFFVRRHITLRLGALVAPVVSFAFLAFCEPMFGFGKFCVQCPG 180
DB 121 LQLLMALECWLSLGHFFVRRHITLRLGALVAPVVSFAFLAFCEPMFGFGKFCVQCPG 180
QY 181 TWCFIQWVHEEGSLVGLSVLYSSLMALVTLVLCNLGAMENLYAMHRRRLQHRPSCT 240
DB 181 TWCFIQWVHEEGSLVGLSVLYSSLMALVTLVLCNLGAMENLYAMHRRRLQHRPSCT 240
QY 241 RDCAEPADGREGASPOLELDHLLALMTVLFTWCSSLFVIYRAYYGAFKVDKVKRNTS 300

Db 241 RDCAEPADGREGASPOLELDHLLALMTVLFTWCSSLFVIYRAYYGAFKVDKVKRNTS 300
QY 301 EEAEEDLRALRFLSVISIVDPWIFIRSPVFRIFFFHKIFIRPLRYRSCNSTNWESSL 359
DB 301 EEAEEDLRALRFLSVISIVDPWIFIRSPVFRIFFFHKIFIRPLRYRSCNSTNWESSL 359
RESULT 4
ADD48182
ID ADD48182 standard; protein; 359 AA.
XX AC ADD48182;
XX 02-DEC-2004 (revised)
XX DT 29-JAN-2004 (first entry)
DE Human Protein Q13258, SEQ ID NO 13980.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS Unidentified.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; Q13258.
XX New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 359 AA;
 Query Match 100.0%; Score 1364; DB 7; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8.1e-187;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPLPSV 60
 DB 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPLPSV 60
 QY 61 FYMLVGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
 DB 61 FYMLVGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
 QY 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFFGKFGVQYCPG 180
 DB 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFFGKFGVQYCPG 180
 QY 181 TWCFIQWVHEGSLSVLGYSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
 DB 181 TWCFIQWVHEGSLSVLGYSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
 QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
 DB 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
 QY 301 EEAEEDLRLALFLSVISIVDPWIFIIFRSPVFRIFHHKIFIRPLRYRSRCSNSTNMESSL 359
 DB 301 EEAEEDLRLALFLSVISIVDPWIFIIFRSPVFRIFHHKIFIRPLRYRSRCSNSTNMESSL 359
 RESULT 5
 ADO29614
 ID ADO29614 standard; protein; 359 AA.
 XX ADO29614;
 DT 29-JUL-2004 (first entry)
 DE Human GPCR PTGDR, SEQ ID NO:716.
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
 KW cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antiulcer; antichryoid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.
 XX Homo sapiens.
 OS
 XX WO2004040000-A2.
 FN
 XX 13-MAY-2004.
 XX
 XX 09-SEP-2003; 2003WO-US028226.
 PF
 XX 09-SEP-2002; 2002US-0409303P.
 PR
 XX 09-APR-2003; 2003US-0461329P.
 XX
 XX (PRIM-) PRIMAL INC.

XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, Meilwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX WPI; 2004-390329/36.
 DR N-PSDB; ADO30026.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX Claim 151; SEQ ID NO 716; 542pp; English.
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 359 AA;
 Query Match 100.0%; Score 1364; DB 8; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8.1e-187;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPLPSV 60
 DB 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPLPSV 60
 QY 61 FYMLVGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
 DB 61 FYMLVGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
 QY 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFFGKFGVQYCPG 180
 DB 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFFGKFGVQYCPG 180
 QY 181 TWCFIQWVHEGSLSVLGYSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
 DB 181 TWCFIQWVHEGSLSVLGYSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
 QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
 DB 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
 QY 301 EEAEEDLRLALFLSVISIVDPWIFIIFRSPVFRIFHHKIFIRPLRYRSRCSNSTNMESSL 359

DB 301 EEADLRALRFLSVISIVDPWIFIRFSPVFRFFHKIFIRPLRYRCSNSTNMESSL 359
 RESULT 6
 ABB12000
 ID ABB12000 standard; peptide; 399 AA.
 AC ABB12000;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human prostaglandin DP receptor homologue, SEQ ID NO:2370.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulation; activin;
 KW inhibin; chemotaxis; chemokines; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; anti-inflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX
 OS Homo sapiens.
 XX
 PN W0200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-457740/49.
 DR
 DR N-PSDB; ABA09244.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 294; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 399 AA;
 Query Match 100.0%; Score 1864; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 9.3e-187;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFFRCQNTTSVEKGNQSAVMGCVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 60
 DB 41 MKSPFFRCQNTTSVEKGNQSAVMGCVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 100
 QY 61 FYMLVCGLTVDLGLKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSST 120
 DB 101 FYMLVCGLTVDLGLKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSST 160
 QY 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFGFVQYCPG 180
 DB 161 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFGFVQYCPG 220
 QY 181 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVLTATVLCNIGMRNLVAMHRRRLQHRPSC 240
 DB 221 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVLTATVLCNIGMRNLVAMHRRRLQHRPSC 280
 QY 241 RDCASPRADGREASPOPLELDHLLALMTVLTWCSLPVIYRAYGAPKDVKEKRTS 300
 DB 281 RDCASPRADGREASPOPLELDHLLALMTVLTWCSLPVIYRAYGAPKDVKEKRTS 340
 QY 301 EEADLRALRFLSVISIVDPWIFIRFSPVFRFFHKIFIRPLRYRCSNSTNMESSL 359
 DB 341 EEADLRALRFLSVISIVDPWIFIRFSPVFRFFHKIFIRPLRYRCSNSTNMESSL 399
 RESULT 7
 AAM79993
 ID AAM79993 standard; protein; 399 AA.
 XX
 AC AAM79993;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3639.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN W0200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.

```
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX N-PSDB; AAK53126.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 403-404; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 399 AA;
XX
XX Query Match 100.0%; Score 1864; DB 4; Length 399;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-187;
XX Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKSPFYRCQNTTSVEKGSNVAAGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKGSNVAAGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 100
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 120
DB 101 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 160
QY 121 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRRLQRHPRSC 240
DB 221 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRRLQRHPRSC 280
QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
DB 281 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 340
QY 301 EEAEEDLRALRFLSVISIVDPWIFIIFRSPVFRIFFFHFIKIFIRPLRYRSCSNSTNMES 359
DB 341 EEAEEDLRALRFLSVISIVDPWIFIIFRSPVFRIFFFHFIKIFIRPLRYRSCSNSTNMES 399
XX
XX RESULT 8
XX ADE09040
XX ID ADE09040 standard; protein; 399 AA.
XX AC ADE09040;
XX
XX 29-JAN-2004 (first entry)
XX
XX Novel protein-related contig polypeptide sequence #106.
XX novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder; contig.
XX
XX Unidentified.
XX
XX WO2003054152-A2.
XX
XX 03-JUL-2003.
XX
XX 10-DEC-2002; 2002WO-US039555.
XX
XX 10-DEC-2001; 2001US-0339739P.
XX 11-DEC-2001; 2001US-0339453P.
XX 14-MAR-2002; 2002US-0365091P.
XX 14-MAR-2002; 2002US-0365384P.
XX 12-APR-2002; 2002US-0372381P.
XX 12-APR-2002; 2002US-0372615P.
XX 22-APR-2002; 2002US-00128558.
XX 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Chosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
XX WPI: 2003-569235/53.
XX
XX New polynucleotides, useful for expressing recombinant proteins for
XX analysis, characterization or therapeutic use, or as markers for tissues
XX in which the corresponding protein is preferentially expressed.
XX
XX Disclosure; SEQ ID NO 2584; 1177pp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel
XX proteins. The DNA and protein sequences of the invention are useful as:
XX markers for tissues in which the corresponding protein is preferentially
XX expressed; as molecular weight markers on gels; as chromosome markers or
XX tags; to identify chromosomes or to map related gene positions; and to
XX compare with endogenous DNA sequences in patients to identify potential
XX genetic disorders. The present amino acid sequence was used in the
XX exemplification of the invention.
XX
XX Sequence 399 AA;
XX
XX Query Match 100.0%; Score 1864; DB 7; Length 399;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-187;
XX Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKSPFYRCQNTTSVEKGSNVAAGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKGSNVAAGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 100
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 120
DB 101 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 160
QY 121 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRRLQRHPRSC 240
DB 221 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMRNLYAMHRRLQRHPRSC 280
QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 300
DB 281 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKDKVKNRTS 340
QY 301 EEAEEDLRALRFLSVISIVDPWIFIIFRSPVFRIFFFHFIKIFIRPLRYRSCSNSTNMES 359
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||||| 341 EEAEDRALRFLVSIVDVFWIFIRFSPVFRIFPHKIFIRPLRYRSCSNSTNMESL 399
|||||
RESULT 9
ADE07993
ID ADE07993 standard; protein; 424 AA.
XX
XX ADE07993;
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #148.
XX
XX novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
XX WO2003054152-A2.
XX
XX 03-JUL-2003.
XX
XX 10-DEC-2002; 2002WO-US039555.
XX
XX 10-DEC-2001; 2001US-0339739P.
XX 11-DEC-2001; 2001US-0339453P.
XX 14-MAR-2002; 2002US-0365091P.
XX 14-MAR-2002; 2002US-0365384P.
XX 12-APR-2002; 2002US-0372381P.
XX 12-APR-2002; 2002US-0372381P.
XX 12-APR-2002; 2002US-0372615P.
XX 22-APR-2002; 2002US-00128558.
XX 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J,
XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
XX Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
XX WPI: 2003-569235/53.
XX N-PSDB; ADE07082.
XX
XX
XX New polynucleotides, useful for expressing recombinant proteins for
XX analysis, characterization or therapeutic use, or as markers for tissues
XX in which the corresponding protein is preferentially expressed.
XX
XX Claim 20; SEQ ID NO 1059; 1177pp; English.
XX
XX
XX The invention comprises the amino acid and coding sequences of novel
XX proteins. The DNA and protein sequences of the invention are useful as
XX markers for tissues in which the corresponding protein is preferentially
XX expressed; as molecular weight markers on gels; as chromosome markers or
XX tags; to identify chromosomes or to map related gene positions; and to
XX compare with endogenous DNA sequences in patients to identify potential
XX genetic disorders. The present amino acid sequence represents a protein
XX of the invention.
XX
XX SQ Sequence 424 AA;
Query Match 94.3%; Score 1757.5; DB 7; Length 424;
Best Local Similarity 89.1%; Pred. No. 1.6e-175;
Matches 344; Conservative 0; Mismatches 1; Indels 41; Gaps 1
QY 1 MKSPFYRCNTTTSVEKGSANVGGVLFTGLLGNLLALGLARSGLWCRRPRLPSPV 60
D6 1 MKSPFYRCNTTTSVEKGSANVGGVLFTGLLGNLLALGLARSGLWCRRPRLPSPV 60
QY 61 FYMLVCGLTVTDLGLKCLLSPVVLAAQAQNSRLRVAPALDNSLCOAFPFMSFFGLSST 120
D6 61 FYMLVCGLTVTDLGLKCLLSPVVLAAQAQNSRLRVAPALDNSLCOAFPFMSFFGLSST 120
QY 121 LQLLAWALECWLSLGHPPFYFRHITLRLGALVAPVVSFAFLAFALPFGMGKFEVQCPG 180
D6 121 LQLLAWALECWLSLGHPPFYFRHITLRLGALVAPVVSFAFLAFALPFGMGKFEVQCPG 180

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FT	Region	185..200 /note= "Prostaglandin D receptor"
FT	FT	195..225
FT	Region	/note= "2 Poly-Immunoglobulin receptor"
FT	Domain	196..219 /label= Transmembrane_domain
FT	FT	236..259
FT	Region	/note= "Prostaglandin D receptor"
FT	Domain	264..283 /label= Transmembrane_domain
FT	FT	280..291
FT	Region	/note= "Prostaglandin D receptor"
FT	Region	297
FT	FT	299
FT	Region	/note= "potential glycosylation site"
FT	Region	312
FT	FT	330
FT	Region	/note= "potential phosphorylation site"
FT	FT	346
FT	Region	/note= "potential phosphorylation site"
XX		
PX	WO200028032-A2.	
XX	18-MAY-2000.	
PD		
XX		
PF	12-NOV-1999;	99WO-US026742.
XX		
PR	12-NOV-1998;	98US-00191280.
PR	07-DEC-1998;	98US-00206647.
PR	08-MAR-1999;	99US-0123404P.
XX		
PA	(INCY-) INCYTE PHARM INC.	
XX		
PI	Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;	
PI	Hillman JL, Bandman O, Azimzai Y, Au-Young J;	
XX		
XX	WPI; 2000-376546/32.	
DR	N-PSDB; AA27056.	
XX		
PT	New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.	
PT		
PS	Claim 1; Page 87-88; 97pp; English.	
XX		
CC	The present sequence is a novel human cell surface receptor protein (HCSRp) designated HCSRp-13. The nucleotide sequence was identified in Incyte Clone 3576503 from the cDNA library BRONN0701, which was made from RNA isolated from bronchial tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to DR prostanoilid receptor g940379. HCSRp and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRp. Such disorders include cancers such as leukaemia and melanoma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as akathesia, Alzheimer's disease, multiple sclerosis and epilepsy. Polynucleotides encoding HSCRps may be used as hybridisation probes to diagnose these conditions. Anti-HCSRp antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRp and for diagnosis of HCSRp-related disorders. HCSRp and its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds	
XX	Sequence 369 AA;	
SQ		
Query Match	84.8%; Score 1580; DB 3; Length 369;	
Best Local Similarity	96.6%; Pred. No. 5.9e-157;	
Matches 308; Conservative	1; Mismatches 6; Indels 4; Gaps 1;	

QY	1	MKSPFYRCQNTTSVEKGNSAVMGVLSTGLLGNLLALGILLARSGLWCSSRRPLRPLPSV	60
Db	1	MKSPFYRCQNTTSVEKGNSAVMGVLFSTGLLGNLLALGILLARSGLWCSSRRPLRPLPSV	60
QY	61	FYMLVCGLTVTDLGKCILLSPVLLAAVAQNRSRLVLPALDNLSCQAFAPFMSFFGLSST	120
Db	61	FYMLVCGLTVTDLGKCILLSPVLLAAVAQNRSRLVLPALDNLSCQAFAPFMSFFGLSST	120
QY	121	LQLLAMALECWLSLGHPPFFYRRHITRLGALVAPVWSAFSLAFCALPFMFGKFVQYCPG	180
Db	121	LQLLAMALECWLSLGHPPFFYRRHITRLGALVAPVWSAFSLAFCALPFMFGKFVQYCPG	180
QY	181	TWCFTOMVHEBGSLSVLGYSVLYSSLMALLVLATVLCNLGAMRNLYAMHRRLOHRPSCT	240
Db	181	TWCFTOMVHEBGSLSVLGYSVLYSSLMALLVLATVLCNLGAMRNLYAMHRRLOHRPSCT	240
QY	241	RDCAEPRADGREASPOPLELDHLILALLMTVLTMCSLPVIYRAYYGAKDVKEKNRTS	300
Db	241	RDCAEPRADGREASPOPLELDHLILALLMTVLTMCSLPVIYRAYYGAKDVKEKNRTS	300
QY	301	EEEDLRALRFLSVISVD 319	
Db	301	EERPPPSL-----ALSICD 315	
RESULT 11			
ADD48180			
ID	ADD48180	standard; protein; 357 AA.	
XX			
AC	ADD48180;		
XX			
DT	02-DEC-2004 (revised)		
DT	29-JAN-2004 (first entry)		
XX			
DE	Rat Protein AAB71762, SEQ ID NO 13878.		
XX			
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;		
KW	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.		
XX			
OS	Rattus norvegicus.		
OS	Unidentified.		
XX			
PN	WO2003016475-A2.		
XX			
PD	27-FEB-2003.		
XX			
PF	14-AUG-2002; 2002WO-US025765.		
XX			
PR	14-AUG-2001; 2001US-0312147P.		
PR	01-NOV-2001; 2001US-0346382P.		
PR	26-NOV-2001; 2001US-0333347P.		
XX			
PA	(GEHO) GEN HOSPITAL CORP.		
PA	(FARB) BAYER AG.		
XX			
PI	Woelf C, D'urso D, Befort K, Costigan M;		
XX			
DR	WPI; 2003-268312/26.		
DR	GENSENK; AAB71762.		
XX			
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.		
PT			
PS	Example 1; Page; 1017pp; English.		
XX			
CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence		

CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 357 AA;

Query Match 74.4%; Score 1386.5; DB 7; Length 357;
Best Local Similarity 76.1%; Pred. No. 1.2e-136;
Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;
QY 6 YRCQNTTSVEKGSNAVMGVLFTGGLGNLLALGLLARSGLWCRRPLRPLPSVFMVLV 65
DB 5 YRCQATWVERGSSATMGVLFAGLLGNLLALVLLARSGLSCRPGLHPPSPVFMVLV 64
QY 66 CGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLLA 125
DB 65 CGTUTVLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLLA 124
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALCPMPGFGKFVQYCPGTWCPI 185
DB 125 MALECWLSLGHPPFYRRHITARGVLVAPVAGFSLAFALCPMPGFGKFVQYCPGTWCPI 184
QY 186 QMVHEGSLVGLVSYLSMALLVLATVLCNLGAMRNLYAMHRLQRHPRSCRDCAE 245
DB 185 QMTKKRSFVIGFVLSYLSMALLVLATVLCNLGAMRNLYAMHRRQHPHRCSDRAQ 244
QY 246 PRADGREALPQLELDHLLLMVLTFTMCSLPVIYRAYYGAFLKDKVKNKTSEAE 305
DB 245 SGSDYRHGSPNLELDHFLVLLATVLTFTMCSLPVIYRAYYGAFLKLV--DRADGDESD 301
QY 306 LRALRFLSVISIDPMTIFIFRSPVPRIPPHKIFIRPLRVSRCSNS--TNWESSL 359
DB 302 LQALRFLSVISIDPMTIFIFRSPVPRIPPHKIFIRPLRVSRCSNS--TNWESSL 357

RESULT 12

AD029615

ID AD029615 standard; protein; 357 AA.

XX AC AD029615;

XX DT 29-JUL-2004 (first entry)

XX DE Mouse GPCR PTGDR, SEQ ID NO:717.

XX

G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; pancreas disorder; testis disorder;
KW skin disorder; stomach disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antinaemic; antiseborrhoeic;

KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX murine; receptor.
OS Mus musculus.
XX WO2004040000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
XX N-PSDB; ADO30316.
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 717; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 357 AA;

Query Match 72.3%; Score 1347.5; DB 8; Length 357;
Best Local Similarity 73.3%; Pred. No. 1.5e-132;
Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;

QY 6 YRCQNTTSVEKGSNAVMGVLFTGGLGNLLALGLLARSGLWCRRPLRPLPSVFMVLV 65

DB 5 YRCQSTWVERGSSATMGVLFAGLLGNLLALVLLARSGLSCRPGLHPPSPVFMVLV 64

QY 66 CGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLLA 125

Db 65 CGLTVTDLGKCLISPNVLAAYAQNSLKEALLPASGNQLCETAFALMSPFGLASTLQLLA 124
QY 126 MALECWLSLGHPPFFYRRHITRLGALVAPVVSFAFALPMFGKFKVQYCPGTWCFT 185
Db 125 MAVECWLSLGHPPFFYRRHITRLGALVAPVVSFAFALPMFGKFKVQYCPGTWCFT 184
QY 186 QMVHEGSLVGLSYSLMALLVLATVLCNLGAMRNLYAMHRLQHRPRSCTRDCAE 245
Db 185 QMTHKERSFSVIGFSVLYSSLMALLVLATVLCNLGAMRNLYAMHRLQHRPRSCTRDCAE 244
QY 246 PRADGREASPOPLEELDHLLALMTVLFMTCSLPLVIYRAYYGAFAKDVKEKNTSBEAE 305
Db 245 SGSDYRHGSLHLELDHFLVLLALMTVLFMTCSLPLVIYRAYYGAFAFAKDVKEKNTSBEAE 301
QY 306 LRALRFLSVISVDPMWIFIRFSPVFRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 359
Db 302 LQALRFLSVISVDPMWIFIRFSPVFRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 357

RESULT 13
ID AAR84708 standard; protein; 357 AA.
XX AAR84708;
AC AAR84708;
DT 06-JUN-1996 (first entry)
XX Prostaglandin D receptor.
DE Prostaglandin D receptor; mouse; PGD-2; therapy; immune activator.
KW Prostaglandin D receptor.
XX Mus musculus.
OS JP07258295-A.
XX 09-OCT-1995.
XX 22-MAR-1994; 94JP-00075382.
XX 22-MAR-1994; 94JP-00075382.
PA (ONONY) ONO PHARM CO LTD.
DR WPI; 1995-380075/49.
DR N-PSDB; AAT05171, AAT05172.
PT Novel murine prostaglandin D receptor - used for the treatment and prevention of diseases caused by PGD-2.
XX Claim 3; Page 6-7; 11pp; Japanese.
XX This sequence represents the murine prostaglandin D receptor. The encoding sequence was obtained through reverse transcription PCR (using the primers represented by AAT05173-T05176). The full length DNA sequence can be used in a vector to transform cells to produce this sequence. This sequence can be used as an agent for the prevention and treatment of diseases caused by excessive production of PGD-2, such as an immune activator and an inhibitor of bleeding
SQ Sequence 357 AA;

Query Match 72.2%; Score 1346.5; DB 2; Length 357;
Best Local Similarity 73.3%; Pred. No. 2e-132;
Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;
QY 6 YRCQNTTSVKEGSAVNGVLFSTGLIGNLLALGLLARSGLGWCRRPLRPLPSVFVMLV 65
Db 5 YRCQNTTSVKEGSAVNGVLFSTGLIGNLLALGLLARSGLGWCRRPLRPLPSVFVMLV 64
QY 66 CGLTVTDLGKCLISPNVLAAYAQNSLKEALLPASGNQLCETAFALMSPFGLASTLQLLA 125
Db 65 CGLTVTDLGKCLISPNVLAAYAQNSLKEALLPASGNQLCETAFALMSPFGLASTLQLLA 124

QY 126 MALECWLSLGHPPFFYRRHITRLGALVAPVVSFAFALPMFGKFKVQYCPGTWCFT 185
Db 125 MAVECWLSLGHPPFFYRRHITRLGALVAPVVSFAFALPMFGKFKVQYCPGTWCFT 184
QY 186 QMVHEGSLVGLSYSLMALLVLATVLCNLGAMRNLYAMHRLQHRPRSCTRDCAE 245
Db 185 QMTHKERSFSVIGFSVLYSSLMALLVLATVLCNLGAMRNLYAMHRLQHRPRSCTRDCAE 244
QY 246 PRADGREASPOPLEELDHLLALMTVLFMTCSLPLVIYRAYYGAFAKDVKEKNTSBEAE 305
Db 245 SGSDYRHGSLHLELDHFLVLLALMTVLFMTCSLPLVIYRAYYGAFAFAKDVKEKNTSBEAE 301
QY 306 LRALRFLSVISVDPMWIFIRFSPVFRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 359
Db 302 LQALRFLSVISVDPMWIFIRFSPVFRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 357

RESULT 14
ID ADP55149 standard; protein; 144 AA.
XX ADP55149;
AC ADP55149;
DT 18-NOV-2004 (first entry)
XX Human PRO protein sequence SEQ ID NO:1125.
DE human; PRO; immune related disease; inflammatory immune response; immune response stimulation; anti-allergic; antianemic; antiarthritic; antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic; antirheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.
XX Homo sapiens.
XX WO2004039956-A2.
XX 13-MAY-2004.
XX 28-OCT-2003; 2003WO-US034381.
XX 29-OCT-2002; 2002US-0422472P.
XX (GETH) GENENTECH INC.
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM; Wood WI, Wu TD;
XX WPI; 2004-376182/35.
XX N-PSDB; ADP55148.
XX New PRO polynucleotides and polypeptides, useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.
XX Claim 1; SEQ ID NO 1125; 3009pp; English.
XX The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptide; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide

CC in a sample suspected of having the polypeptide; (11) a method of
 CC diagnosing an immune related disease or an inflammatory immune response
 CC in mammal; (12) a method of identifying a compound that inhibits or
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide
 CC ; and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have anti-allergic, antianemic, antiarthritic,
 CC antiachmatic, antidiabetic, antiinflammatory, antiporiatic,
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC virucide activities, and can be used in gene therapy. The nucleic acid
 CC (I) and the encoded polypeptides, compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO protein from the present invention.

XX SQ Sequence 144 AA;

Query Match 40.3%; Score 752; DB 8; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.9e-70;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 LCNIGMNLVAMHRLQHRPSTCTDCAEPRADGREGASPOLELDHLLALLMTVLFT 275
 Db 1 LCNIGMNLVAMHRLQHRPSTCTDCAEPRADGREGASPOLELDHLLALLMTVLFT 60

Qy 276 MCSLPVIYRAYYGAFKDVKEKNTSEAEIDLALRFLSVISIDVPWIFIRSPVFRIF 335
 Db 61 MCSLPVIYRAYYGAFKDVKEKNTSEAEIDLALRFLSVISIDVPWIFIRSPVFRIF 120

Qy 336 HKIFIRPLRYRSCSNSTNMESL 359
 Db 121 HKIFIRPLRYRSCSNSTNMESL 144

RESULT 15

ADO29619
 ID ADO29619 standard; protein; 362 AA.

AC ADO29619;

XX 29-JUL-2004 (first entry)

DE Mouse GPCR PTGER2, SEQ ID NO:721.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytosatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; receptor.

XX Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI: 2004-390329/36.

DR N-PSDB; ADO30318.

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 721; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: the full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 362 AA;

Query Match 38.0%; Score 707.5; DB 8; Length 362;
 Best Local Similarity 44.5%; Pred. No. 2.9e-65;
 Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;

Qy 8 CQNTTSVEKGN SAVMGVLPSTGLLGNLLALGALLARSLG--WCSRRPLPLPSVFYMLV 65

Db 14 CKSRQWLGGESPAISSVMFSAGVLGNLIALALLARRWRGDTGCSAGS-RTSLSLFHLV 72

Qy 66 CGLTVDLGLCKLLSPVLLAAVAQNLSRLVAPALDNLCOAFPMFSFGLSSTQLLA 125

Db 73 TELVLTLDLGTCLISPVLLASYSRNTLVALAP-ESHACTYFAFTWTFSLATMLMFA 130

Qy 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSAPSLAFALCPMGFGKVOYCPGTWCPI 185

Db 131 MALERYLSIGYPFYRRHLSSRGGLAVLPVIYGASLLFCSLLPLNLYGEYVOYCPGTWCPI 190

Qy 186 QMVEEGSLSVLGYSVLVYSSLMALLVATVLCNLGAMRNLYAMHRLQHRPSCTRDCAE 245

Db 191 R--HGR-----TAYLQYATMLLLLIVAVLACNISVLNLIRHRSRR--SRCGLSGSS 241

Qy 246 PRADG--REASQPLEDLHLLALLMTVLTWMLCVIYRAYYGAFKDVKEKNTSEE 302

Db 242 LRPGSGRRRGERTSMAEETHLLILLAIMITFAICSLPPTFIYMETSTSLKEK----- 295

Qy 303 AEDLRALRFLSVISIDVPWIFIRSPVFRIFPHKIFIR-PLRYRSCSNSTNMESS 358

Db 296 -WDLRALRFLSVNSIIDPWVFAILRPPVLFRLMESVLCRCRTSLRTOEAAQOTSCSTQSS 351

Search completed: April 22, 2005, 21:27:24
Job time : 66.771 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 20:46:09 ; Search time 17.5389 Seconds
(without alignments)
1969.437 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFYRCQNTTSVEKNSA.....IRPLVRSRCSNTNWESSL 359
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1864	100.0	359	2 I39153	prostanoid DP rece
2	943	50.6	231	2 I59269	prostaglandin D re
3	707.5	38.0	362	2 S66674	prostaglandin E re
4	689	37.0	358	2 I38920	prostaglandin E2 r
5	688	36.9	358	2 S51312	EP2 prostaglandin
6	597	32.0	386	2 A57066	prostacyclin recep
7	596.5	32.0	417	2 A54416	prostacyclin recep
8	585.5	31.4	416	2 S52078	prostacyclin - rat
9	458.5	24.6	513	2 A46638	prostaglandin E re
10	452.5	24.3	488	2 JC2241	prostaglandin E re
11	443	23.8	488	2 A53572	prostaglandin E2 r
12	314	16.8	362	2 S48689	prostaglandin E(2)
13	313.5	16.8	366	2 S51280	EP3-alpha receptor
14	308	16.5	365	2 A42414	prostaglandin E re
15	308	16.5	365	2 JN0693	prostaglandin E2 r
16	307.5	16.5	361	2 A45211	prostaglandin E re
17	307.5	16.5	364	2 JC2115	prostaglandin E re
18	307.5	16.5	364	2 S65009	prostaglandin E re
19	298.5	16.0	361	2 A53216	prostaglandin E2 r
20	298.5	16.0	393	2 S51318	prostaglandin E re
21	297.5	16.0	390	2 S43375	prostaglandin E re
22	297.5	16.0	390	2 S51313	prostaglandin E re
23	296.5	15.9	411	2 B53216	prostaglandin E2 r
24	294	15.8	388	2 S51316	prostaglandin E re
25	294	15.8	388	2 I38750	prostaglandin recep
26	293.5	15.7	365	2 I3748	prostaglandin recep
27	293.5	15.7	365	2 S51315	prostaglandin E re
28	292.5	15.7	367	2 JC2056	prostaglandin E2 r
29	292.5	15.7	369	2 A53599	thromboxane A-2 re

30	292.5	15.7	407	2 T02670	probable thromboxa
31	291.5	15.6	374	2 I38747	prostaglandin recep
32	291.5	15.6	374	2 S51317	prostaglandin E re
33	291.5	15.6	425	2 S51319	prostaglandin E re
34	289.5	15.5	343	2 A49117	thromboxane A2 rec
35	286.5	15.4	385	2 S36765	prostaglandin E re
36	284.5	15.3	362	2 S36766	prostaglandin E re
37	284.5	15.3	387	2 S36767	prostaglandin E re
38	284.5	15.3	417	2 S36764	prostaglandin E re
39	266	14.3	341	2 I55623	thromboxane A2 rec
40	257	13.8	341	2 JH0606	thromboxane A2 rec
41	255.5	13.7	402	1 A49690	prostaglandin E re
42	247.5	13.3	76	2 I80042	prostaglandin D re
43	246	13.2	405	2 S66525	prostanoid recepto
44	241	12.9	366	2 A49877	prostaglandin F re
45	238	12.8	366	2 I53488	prostaglandin F2 a

ALIGNMENTS

RESULT 1
I39153
prostanoid DP receptor - human
N;Alternate names: prostaglandin D2 receptor
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: I39153; I39150; I39149
R;Boile, Y.; Sawyer, N.; Slipetz, D.M.; Metters, K.M.; Abramovitz, M.
J. Biol. Chem. 270, 18910-18916, 1995
A;Title: Molecular cloning and characterization of the human prostanoid DP receptor.
A;Reference number: I39149; MUID:95370201; PMID:7642548
A;Accession: I39153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q13258; EMBL:U31332; NID:g940378; PIDN:AAC50178.1; PID:g9403
A;Accession: I39150
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 216-359 <RES2>
A;Cross-references: EMBL:U31099; NID:g940376; PIDN:AAC50177.1; PID:g940377
A;Accession: I39149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 283-328 <RES3>
A;Cross-references: EMBL:U31098; NID:g940374; PIDN:AAC50176.1; PID:g940375
C;Genetics:
A;Gene: GDB:PTGDR
A;Cross-references: GDB:681159
A;Map position: 10q23-10q23
C;Superfamily: prostaglandin E receptor EP1
C;Keywords: G protein-coupled receptor

Query Match	100.0%;	Score 1864;	DB 2;	Length 359;
Best Local Similarity	100.0%;	Pred. No. 4.1e-153;		
Matches	359;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRPLRPLPSV	60	
Db	1	MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRPLRPLPSV	60	
Qy	61	FYMLVGLTVTDLLGKLLSPVVLAAAYQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSST	120	
Db	61	FYMLVGLTVTDLLGKLLSPVVLAAAYQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSST	120	
Qy	121	LQLLAMALECWLGLGHPFFRRHITLRLGALVAPVVSFAFSLAFALPFMGFGFVQYCPG	180	
Db	121	LQLLAMALECWLGLGHPFFRRHITLRLGALVAPVVSFAFSLAFALPFMGFGFVQYCPG	180	
Qy	181	TWCFIQMVHEEGSLSVLGSVLYSSLMALLVTLVLCNIGAMENLYAMHRRLLQRHRSCT	240	
Db	181	TWCFIQMVHEEGSLSVLGSVLYSSLMALLVTLVLCNIGAMENLYAMHRRLLQRHRSCT	240	

QY 241 RDCAEPRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNTS 300
Db 241 RDCAEPRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNTS 300
QY 301 EEAEDLRAFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESSL 359
Db 301 EEAEDLRAFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESSL 359
RESULT 2
I59269
prostaglandin D receptor (prostanoid DP receptor) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Sep-1998
C:Accession: I59269
R:Hirata, M.; Kakizuka, A.; Aizawa, M.; Ushikubi, F.; Narumiya, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 11192-11196, 1994
A:Title: Molecular characterization of a mouse prostaglandin D receptor and functional e
A:Reference number: I59269; MUID:95062232; PMID:7972033
A:Accession: I59269
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-231 <RES>
A:Cross-references: GB:D29764; NID:9577718; PID:9577719
C:Superfamily: prostaglandin E receptor EP1
Query Match 50.6%; Score 943; DB 2; Length 231;
Best Local Similarity 79.2%; Pred. No. 6.4e-74;
Matches 179; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 6 YRCQNTTSVEKGSNAVMGGVLFSTGLGNLLALGLLARSGLGCRPLPLPSVFMVLV 65
Db 5 YRCQNTTSVEKGSNAVMGGVLFSTGLGNLLALGLLARSGLGCRPLPLPSVFMVLV 64
QY 66 CGLTVTDLGKCLLSPVLAAYQAQRSLRLVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 65 CGLTVTDLGKCLLSPVLAAYQAQRSLRLVLPALDNLSCQAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCPI 185
Db 125 MAVECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCPI 184
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 231
Db 185 QMTHKERSFSGVIGSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 230
RESULT 3
S66674
prostaglandin E receptor EP2 subtype - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66674
R:Katayama, M.; Nishigaki, N.; Sugimoto, Y.; Morimoto, K.; Negishi, M.; Narumiya, S.; I
FEBS Lett. 372, 151-156, 1995
A:Title: The mouse prostaglandin E receptor EP(2) subtype: cloning, expression, and Nor
A:Reference number: S66674; MUID:96000196; PMID:7556658
A:Accession: S66674
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <KAT>
A:Cross-references: UNIPROT:Q62053; EMBL:D50589; NID:g829048; PID:g8290
C:Superfamily: prostaglandin E receptor EP1
Query Match 38.0%; Score 707.5; DB 2; Length 362;
Best Local Similarity 44.5%; Pred. No. 2e-53;
Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;
QY 8 QMNTTSVEKGSNAVMGGVLFSTGLGNLLALGLLARSGLG--WCSRRPLPLPSVFMVLV 65
Db 14 CKSQMLLSGSPAISSVMFSGVGLGNLLALGLLARSGLG--RTSISLFLVLV 72

QY 66 CGLTVTDLGKCLLSPVLAAYQAQRSLRLVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 73 TELVTLDTLGLTCLISPVLAASRNQTLVALAP--ESHACTYFAFTWTFSLATMLMFLA 130
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCPI 185
Db 131 MALERYLSLGHPPFYRRHLSRGGGLAVLPVYASLLFCSLPLNLYGEVQYCPGTWCPI 190
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 245
Db 191 R--HGR-----TAYLQYATMLLLLVAVLACNISVILNLRHRRSR--SRCGLSGSS 241
QY 246 PRADG---REASQPUELDHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNTSEE 302
Db 242 LRCPGSRRGERTSMAEETHLLLLAIMTITFAICSLPFTIFAYMDETSLSEK----- 295
QY 303 AEDLRAFLSVISIVDPWIFIRSPVFRIFHHKIFIR-PLRYRSCSNSTNMESS 358
Db 296 -WDLRALRFLSVNSIIDPWFVFAIRLPPVLRMLRSLVLCRTSLRTQEAQOOTSCTSQSS 351
RESULT 4
I38920
prostaglandin E2 receptor - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I38920
R:Regan, J.W.; Bailey, T.J.; Pepperl, D.J.; Pierce, K.L.; Bogardus, A.M.; Donello, J.E.;
Mol. Pharmacol. 46, 213-220, 1994
A:Title: Cloning of a novel human prostaglandin receptor with characteristics of the pha
A:Reference number: I38920; MUID:94359483; PMID:8078484
A:Accession: I38920
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-358 <RES>
A:Cross-references: UNIPROT:P43116; EMBL:U19487; NID:g639719; PID:AAA61681.1; PID:g6326
C:Superfamily: prostaglandin E receptor EP1
Query Match 37.0%; Score 689; DB 2; Length 358;
Best Local Similarity 43.7%; Pred. No. 7.8e-52;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;
QY 8 QMNTTSVEKGSNAVMGGVLFSTGLGNLLALGLLARSGLG--WCSRRPLPLPSVFMVLV 65
Db 13 CETROWLPGESPAISSVMFSGVGLGNLLALGLLARSGLG--WCSRRPLPLPSVFMVLV 71
QY 66 CGLTVTDLGKCLLSPVLAAYQAQRSLRLVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 72 TELVTLDTLGLTCLISPVLAASRNQTLVALAP--ESHACTYFAFTWTFSLATMLMFLA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCPI 185
Db 130 MALERYLSLGHPPFYRRVSASGGLAVLPVYASLLFCSLPLDLYGQYVQYCPGTWCPI 189
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 245
Db 190 R--HGR-----TAYLQYATMLLLLVAVLACNISVILNLRHRRSR--SRCGPSLGS 240
QY 246 ----PRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNTSE 301
Db 241 GRGPGARRRGERSVMAEETHLLLLAIMTITFAVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DLRALRFLSVISIVDPWIFIRSPVFRIFHHKIFIR-PLRYRSCSNSTNMES 357
Db 292 RKEKWDQLARFLVNSIIDPWFVFAIRLPPVLRMLRSLVLCRTSLRTQDTQTSCSTQS 350
RESULT 5
S51312
EP2 prostaglandin receptor - human
C:Species: Homo sapiens (man)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51312

R;Oakley, C.J.

Submitted to the EMBL Data Library, January 1995

A;Reference number: S51312

A;Accession: S51312

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-358 <OK>

A;Cross-references: UNIPROT:P43116; EMBL:X83868; NID:9633205; PIDN:CAA58749.1; PID:96332

C;Superfamily: prostaglandin E receptor EPI

Query Match 36.9%; Score 688; DB 2; Length 358;
Best Local Similarity 43.7%; Pred. No. 9.5e-52;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRPLRLPLPSVFMVLY 65

DB 13 CETRWMLPPGESPAISSWMFSGVGLNLLALARRWRGDVGSAGRRSSL-SLFHLV 71

QY 66 CGITVTDLLGKCLLSPVLAAYQNRSLRVLAALDNLSCQAFPMSPFGLSSTLQLLA 125

DB 72 TELVFTDGLTCLISPVLAAYQNRSLRVLAALDNLSCQAFPMSPFGLSSTLQLLA 129

QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSAPSLAFPCALPMGFGKFGVQYCPGTWCFF 185

DB 130 MALERYLSIGHPPFYQRRVSRSGGLAVLPVYAVSLFLFCSEPLLDYQYQYCPGTWCFF 189

QY 186 QMVEHGSLSVLGYSVLYSSIMALLVLTATVLCNLGMNLYAMHRLQRHPRSCTRDCAE 245

DB 190 R--HGR-----TAYLQYATLLLLIIVSLACNFSVLNLRWHRRSR--SRCGPSLGS 240

QY 246 ----PRADGREASQPLELDHLLALMTVLCMLSPVIRAYGAFKDVKEKNTSE 301

DB 241 GRGGPGARRGERVSMAEEDHLILLAITTFVAVCSLPTIFAY-----MNETSS 291

QY 302 EAE--DLRALRFLSVISIDPWIFIFRSPVERIFFKIFIR-PLVRSRCSNSTMES 357

DB 292 RKEKWDQLARFLSINSIIDPWIFVFAIRPPVLRMRSLVLCRISLRTQDATQISCSQS 350

RESULT 6

A57066

prostaglandin receptor - human

C;Alternate names: prostaglandin I2 receptor; prostanoind IP receptor

C;Species: Homo sapiens (man)

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C;Accession: A57066; S43952; A53587; I52867

R;Ogawa, Y.; Tanaka, I.; Inoue, M.; Yoshitake, Y.; Isse, N.; Nakagawa, O.; Usui, T.; Ito

Genomics 27, 142-148, 1995

A;Title: Structural organization and chromosomal assignment of the human prostacyclin re

A;Reference number: A57066; MUID:95394450; PMID:7665161

A;Accession: A57066

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-386 <OK>

A;Cross-references: UNIPROT:P43119; GB:D38127; GB:D38128; NID:g1019364; PIDN:BA07325.1;

R;Katsuyama, M.; Sugimoto, Y.; Namba, T.; Irie, A.; Negishi, M.; Narumiya, S.; Ichikawa,

FEBS Lett. 344, 74-78, 1994

A;Title: Cloning and expression of a cDNA for the human prostacyclin receptor.

A;Reference number: S43952; MUID:94237286; PMID:7514139

A;Accession: S43952

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-386 <OK>

A;Cross-references: EMBL:D25418; NID:g467509; PIDN:BA005008.1; PID:g467510

R;Boie, Y.; Rushmore, T.H.; Darmon-Goodwin, A.; Grygorczyk, R.; Slipeez, D.M.; Metters,

J. Biol. Chem. 269, 12173-12178, 1994

A;Title: Cloning and expression of a cDNA for the human prostanoind IP receptor.

A;Reference number: A53587; MUID:94216334; PMID:7512962

A;Accession: A53587

A;Molecule type: mRNA

A;Residues: 1-386 <BOI>

A;Cross-references: GB:I29016; NID:g495042; PIDN:AAA36448.1; PID:g495043

R;Nakagawa, O.; Tanaka, I.; Usui, T.; Harada, M.; Sasaki, Y.; Itoh, H.; Yoshimasa, T.; N

Circulation 90, 1643-1647, 1994

A;Title: Molecular cloning of human prostacyclin receptor cDNA and its gene expression i

A;Reference number: I52867; MUID:95008086; PMID:7923647

A;Accession: I52867

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-386 <RES>

A;Cross-references: GB:D29634; NID:g577629; PIDN:BAA06110.1; PID:g577630

C;Genetics:

A;Gene: GDB:PTGIR

A;Cross-references: GDB:373439; OMIM:600022

A;Map position: 19q13.3-19q13.3

C;Superfamily: prostaglandin E receptor EPI

C;Keywords: transmembrane protein

Query Match 32.0%; Score 597; DB 2; Length 386;
Best Local Similarity 42.3%; Pred. No. 7.1e-44;
Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWSRRPLRLPLPSVFMVLYCG 67

DB 5 CRNLTVRGSVGPATSTLMFVAGVGNLALGILS-----ARRPAR--PSAFVAVLTG 55

QY 68 LTVTDLLGKCLLSPVLAAYQNRSLRVLA---PALDNLSCQAFAPFMSFGLSSTLQLL 124

DB 56 LAATDGLTGLSPAVFVAYARNSSLGLARGGPA-----LCDAPAFAMTFFGLASMLILF 111

QY 125 AMALECWLSLGHPPFYRRHITRLGALVAPVVSAPSLAFPCALPMGFGKFGVQYCPGTWCFF 184

DB 112 AMAVERCLALSHPLYLAQLDGPRCARLALPAIYAFVCLFALPLGLGQHQYCPGSCWCP 171

QY 185 IQM--VHEGSLSVLGYSLVLYSSIMALLVLTATVLCNLGMNLYAMHRLQRHPRSCTRD 242

DB 172 LRMRWAPGGA---AFSLAYAGLVALLVAALFCLNGSVTLSCRMVYRQQRHOGS---- 223

QY 243 CAEPRADGREASQPL---EELDHLILLALMTVLCMLSPVIRAYGAFKDVKEKNT 299

DB 224 -----LGRPRRTGEDEVLDHLLALMTVVMVAVCSLPLTRCTQAVP-----DS 268

QY 300 SEEAEDLRALRFLSVISIDPWIFIFRSPVFR 332

DB 269 SSEMGDLALAFRFAFNPILDPMVILFRKAVFO 301

RESULT 7

A54416

prostaglandin receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000

R;Namba, T.; Oida, H.; Sugimoto, Y.; Kakizuka, A.; Negishi, M.; Narumiya, S.

J. Biol. Chem. 269, 9986-9992, 1994

A;Title: cDNA cloning of a mouse prostacyclin receptor. Multiple signaling pathways and

A;Reference number: A54416; MUID:94193694; PMID:7511597

A;Accession: A54416

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-417 <NAM>

A;Cross-references: GB:D26157; NID:g493687; PIDN:BAA05144.1; PID:g493688

C;Superfamily: prostaglandin E receptor EPI

Query Match 32.0%; Score 596.5; DB 2; Length 417;

Best Local Similarity 42.8%; Pred. No. 8.5e-44;

Matches 139; Conservative 43; Mismatches 114; Indels 29; Gaps 7;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWSRRPLRLPLPSVFMVLYCG 67

DB 35 CWNITTVQSVGPATSTLMFVAGVGNLALGILG-----ARR--RSHPSAFVAVLTG 85

QY 68 LTVTDLLGKCLLSPVLAAYQNRSLRVLAALDNLSCQAFAPFMSFGLSSTLQLLAWA 127

DB 86 LAVTDLLGTCFLSPAVFVAYARNSSLGLAHG-GTLMCDTFAFAMTFFGLASTLILFAMA 144

QY 128 LECWLSLGHGHPFFRRHITLRLGALVAPVVSARSLAFALCFALPFMGFGKVFQVCPGTWCPIOM 187
Db 145 VERCLALSHPLYAQLDGPRCARFALPSIYAFCLFCSPLLLGLGHEHQYCPGSGWCFIRM 204
QY 188 VHEEGSLVGLGYSLVSSYLLMALVLTATVLCNLGAMRNLYAMHRRLOHPRSCRTDCAEP 247
Db 205 --RSAQPGGCAFLAYASLWALLVTSIFFCNGSVTLISLHYMYRQRRHGSFV----PT 257
QY 248 ADGREASPOPLELDLHLLALMTVLFMTCSLPIVYRAYGAFKDVKEKRTSEBAEDLR 307
Db 258 SRARE-----DEVYHLILALMTVIMAVCSLPLMIRGETQAIAP-----DSREMGDL 305
QY 308 ALRFLSVISIVDPWFIFRSPVFR 332
Db 306 AFRFNAFNILDPWFILFRKAVFQ 330

RESULT 8
S52078
prostaglandin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52078
R;Sasaki, Y.; Usui, T.; Tanaka, I.; Nakagawa, O.; Sando, T.; Takahashi, T.; Namba, T.; N
Biochim. Biophys. Acta 1224, 601-605, 1994
A;Title: Cloning and expression of a cDNA for rat prostacyclin receptor.
A;Reference number: S52078; MUID:95101758; PMID:7803522
A;Accession: S52078
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <SAS>
A;Cross-references: UNIPROT:P43253; GB:D28966; NID:9602775; PIDN:BA06091.1; PID:9602776
C;Superfamily: prostaglandin E receptor EPI

Query Match 31.4%; Score 585.5; DB 2; Length 416;
Best Local Similarity 42.6%; Pred. No. 7.5e-43;
Matches 139; Conservative 44; Mismatches 112; Indels 31; Gaps 8;

QY 8 QNTTSVEKGNASVMGVLFTSLGGLNLLALGALLARSLGLWCSSRRPLPLPSVFMVLCG 67
Db 34 CWNITVQDSVGPATSTLMFVAGVGNLGLILG-----ARR--RSHPSAFALVLTG 84
QY 68 LTVTDLGLKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLAWA 127
Db 85 LAVTDLTGTCFLSPAFVATARNSSLLGLAHG-GTMLCDTFAFAMIFFGLASTLILFAMA 143
QY 128 LECWLSLGHGHPFFRRHITLRLGALVAPVVSARSLAFALCFALPFMGFGKVFQVCPGTWCPIOM 187
Db 144 VERCLALSHPLYAQLDGPRCARLALPAIYAFCLFCSPLLLGLGHEHQYCPGSGWCFIRM 203
QY 188 -VHEEGSLVGLGYSLVSSYLLMALVLTATVLCNLGAMRNLYAMHRRLOHPRSCRTDCAEP 246
Db 204 RSPQPGCA---FSLAYASLWALLVTSIFFCNGSVTLISLCHMYRQRRHGSFV-----P 255
QY 247 ADGREASPOPLELDLHLLALMTVLFMTCSLPIVYRAYGAFKDVKEKRTSEBAEDL 306
Db 256 TSARE-----DEVYHLILALMTGIMAVCSLPLTIRGTQAIAP-----DSREMGDL 303
QY 307 RALRFLSVISIVDPWFIFRSPVFR 332
Db 304 HAFRFNAFNILDPWFILFRKAVFQ 329

RESULT 9
A46638
prostaglandin E receptor EP2 subtype - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46638
R;Honda, A.; Sugimoto, Y.; Namba, T.; Watabe, A.; Irie, A.; Negishi, M.; Narumiya, S.; I
J. Biol. Chem. 268, 7759-7762, 1993
A;Title: Cloning and expression of a cDNA for mouse prostaglandin E receptor EP2 subtype
A;Reference number: A46638; MUID:93216741; PMID:8385118

A;Accession: A46638
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-513 <HON>
A;Cross-references: UNIPROT:P32240; GB:D13458; NID:G303699; PIDN:BA002714.1; PID:G303700
A;Experimental source: mastocytoma P-815 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:128997, NCBIP:128998)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.6%; Score 458.5; DB 2; Length 513;
Best Local Similarity 31.9%; Pred. No. 8.2e-32;
Matches 118; Conservative 65; Mismatches 132; Indels 55; Gaps 11;

QY 1 MXPFPYRCQNTTSVEKGNASV-MGGVLFSTGLLGNLLALGALLARSLGLWCSSRRPLPLPS 59
Db 26 MSIPGVNASFSSTPERLNSPVTIPAVMFIFGVVGNLVAIVLCK-----SRKEQK--ET 77
QY 60 VFYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAPFMSFFGLSS 119
Db 78 TFYTLVCGLAVTDLLGLTLLVSPVTIATYMKGQ-----WPG-DOALCDYSTFILLFFGLSG 131
QY 120 TLQLLAWALECWLSLGHGHPFFRRHITLRLGALVAPVVSARSLAFALCFALPFMGFGKVFQVCP 179
Db 132 LSIICAMSIERYLAINHAYFYSHYVDKRLAGLTFAIYASNVLFALPNNMGLGRSERQYP 191
QY 180 GTWCFTQVHEEGSLVLCY---SVLYSSLMALLVLTATVLCNLGAMRNLYAMHRRLOH-- 234
Db 192 GTWCFTI-----DWTNTVATYAAAFSYNYAGFSFLILATVLCNVLVGALLRMHRRQMRRT 246
QY 235 -----HPRSCRTDCAEPADGREASPOPLE-----ELDHLLALLALMT 271
Db 247 SLGTEQHAAAAAASVACRGHAGASPALQRLSDFRFRSFPRIAGAEIQWILLIATS 306
QY 272 VLFTMCSLPIVYRAYGAFK---VKEKRTSEBAEDLRALRFLSVISIVDPWFIFR 328
Db 307 LVVLICSLPLVVRVFNQLYQPNVVKD1SRN-----PDLOAIRIASVNPILDPIYILLRK 362
QY 329 PVFRIFFHKI 338
Db 363 TVLSKAIEKI 372

RESULT 10
JC2241
prostaglandin E receptor EP2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2241
R;Sando, T.; Usui, T.; Tanaka, I.; Mori, K.; Sasaki, Y.; Fukuda, Y.; Namba, T.; Sugimoto, Y.
Biochem. Biophys. Res. Commun. 200, 1329-1333, 1994
A;Title: Molecular cloning and expression of rat prostaglandin E receptor EP2 subtype.
A;Reference number: JC2241; MUID:94241990; PMID:8185583
A;Accession: JC2241
A;Molecule type: mRNA
A;Residues: 1-488 <SAN>
A;Cross-references: UNIPROT:P43114; DBJ:D28860; NID:G516827; PIDN:BA006011.1; PID:G516828
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;20-44/Domain: transmembrane #status predicted <TM1>
F;56-79/Domain: transmembrane #status predicted <TM2>
F;97-116/Domain: transmembrane #status predicted <TM3>
F;136-160/Domain: transmembrane #status predicted <TM4>
F;185-211/Domain: transmembrane #status predicted <TM5>
F;271-298/Domain: transmembrane #status predicted <TM6>
F;316-335/Domain: transmembrane #status predicted <TM7>
F;7.177/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,262,373,374/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #

Query Match 24.3%; Score 452.5; DB 2; Length 488;
Best Local Similarity 32.7%; Pred. No. 2.6e-31;
Matches 121; Conservative 66; Mismatches 128; Indels 55; Gaps 13;

EP3-alpha receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 23-Jul-1999
C:Accession: S51280
R:Neuschaefer-Rube, F.; de Vries, C.; Haenecke, K.; Jungermann, K.; Püeschel, G.P.
submitted to the EMBL Data Library, January 1995
A:Reference number: S51280
A:Accession: S51280
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-366 <NEU>
A:Cross-references: EMBL:X83855; NID:g633623; PIDN:CAA58735.1; PID:g633624
C:Superfamily: prostaglandin E receptor EP1

Query Match 16.8%; Score 313.5; DB 2; Length 366;
Best Local Similarity 28.8%; Pred. No. 1.9e-19;
Matches 105; Conservative 61; Mismatches 148; Indels 53; Gaps 13;

QY 10 NTTSEKGNVAVGG---VLFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 66
DB 16 NQSSAADGCGSVSVAPFIMTMTVTFVGNALMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKLLSPVLAAYQNRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
DB 71 WLALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCCTFFGLTMTVFGSLSLVASAM 128

QY 127 ALECWLSLGHPPFFRHHITRLGALVAPVVSFAFLAFALPFGMGKGFVQVCPGTWCFI- 185
DB 129 AVERALAIRAPHWYASHMKTRATRAVLVGLVWLSVLAFLPVLGVRYSVQWPGTWCFS 188

QY 186 -----QMVHEGSLSVLGVSYSLLMALLVLATVLCNLGAMRNLYAMHRRRLQRHP 237
DB 189 TGPAGNETDSAREPGSA---FASAFACGLGALLVVTFACTNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASQPQLELDHLLALMTVLTMCSPVIVRAYYGAFKDV 294
DB 236 RCRAKAAASQSAQWGRITTAIQ-----LMGIMCVL-SVCWSPLLIMLMKMFNQMS 288

QY 295 E---KNTSEAE---DLRALRFLSVISIVDPWIFIRFSPVPRIFPHKIFIRPLRYRSR 348
DB 289 VEQCKTQMGKEKCNFSFLIAVRLASNLQILDPPWVYLLLRKILLRKFCQ----IRD--HTNY 343

QY 349 CSNSTNM 355
DB 344 ASSSTSL 350

RESULT 14
A42414
Prostaglandin E receptor EP3 subtype - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42414
R: Sugimoto, Y.; Namba, T.; Honda, A.; Hayashi, Y.; Negishi, M.; Ichikawa, A.; Narumiya, J. Biol. Chem. 267, 6463-6466, 1992
A:Title: Cloning and expression of a cDNA for mouse prostaglandin E receptor EP3 subtype
A:Reference number: A42414; MUID:92202182; PMID:1372606
A:Accession: A42414
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-365 <SUG>
A:Cross-references: UNIPROT:P10557; GB:D10204; NID:g220571; PIDN:BAA01051.1; PID:g220572
A:Note: sequence extracted from NCBI backbone (NCBIN:89525, NCBI:P:89530)
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 16.5%; Score 308; DB 2; Length 365;
Best Local Similarity 28.5%; Pred. No. 5.5e-19;
Matches 105; Conservative 66; Mismatches 139; Indels 58; Gaps 15;

QY 10 NTTSEKGNVAVGGV-LFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 68
DB 18 SSTTDCGVSVAFFIMTMTVTFVGNALMLLVRS-----YRRRESKRKKSFLLCIG 72

QY 69 TWTDLGKLLSPVLAAYQNRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAMAL 128
DB 73 ALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCCTFFGLTMTVFGSLSLVASAMAV 130

QY 129 ECWLSLGHPPFFRHHITRLGALVAPV---VSASFSLAFALPFGMGKGFVQVCPGTWCFI 185
DB 131 ERALAIRAPHWYASHMKTR---ATFVLLGVWLSVLAFLPVLGVRYSVQWPGTWCFI 186

QY 186 QM-----VHEEGSLSVLGVSYSLLMALLVLATVLCNLGAMRNLYAMHRRRLQRHP 236
DB 187 STGPAGNETDPAEPGSA---FASAFACGLGALLVVTFACTNLATIKALVS----- 234

QY 237 RSCTRDCAEPRAD---GREASQPQLELDHLLALMTVLTMCSPVIVRAYYGAFKDV 293
DB 235 -RCRAKAAVSQSAQWGRITTAIQ-----LMGIMCVL-SVCWSPLLIMLMKMFNQM 286

QY 294 KE---KNTSEAE---DLRALRFLSVISIVDPWIFIRFSPVPRIFPHKIFIRPLRYRS 347
DB 287 SVEQCKTQMGKEKCNFSFLIAVRLASNLQILDPPWVYLLLRKILLRKFCQ----IRD--HTN 341

QY 348 RCSNSTNM 355
DB 342 YASSSTSL 349

RESULT 15
JN0693
Prostaglandin E2 receptor EP3 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JN0693; PN0551; S40683
R:Takeuchi, K.; Abe, T.; Takahashi, N.; Abe, K.
Biochem. Biophys. Res. Commun. 194, 885-891, 1993
A:Title: Molecular cloning and intrarenal localization of rat prostaglandin E2 receptor
A:Reference number: S40683; MUID:93343951; PMID:8393672
A:Accession: JN0693
A:Molecule type: mRNA
A:Residues: 1-365 <TAK>
A:Cross-references: UNIPROT:P34980; GB:D14869; NID:g467530; PIDN:BAA03585.1; PID:g467531
A:Accession: PN0551
A:Molecule type: protein
A:Residues: 336-365 <TAK>
C:Comment: This protein exerts an inhibitory effect on water and sodium reabsorption by
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:31-55/Domain: transmembrane #status predicted <TM1>
F:69-89/Domain: transmembrane #status predicted <TM2>
F:109-130/Domain: transmembrane #status predicted <TM3>
F:152-173/Domain: transmembrane #status predicted <TM4>
F:204-229/Domain: transmembrane #status predicted <TM5>
F:260-283/Domain: transmembrane #status predicted <TM6>
F:304-325/Domain: transmembrane #status predicted <TM7>
F:16,193/Binding site: carboxylate (Asn) (covalent) #status predicted
F:59,64/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 16.5%; Score 308; DB 2; Length 365;
Best Local Similarity 28.6%; Pred. No. 5.5e-19;
Matches 106; Conservative 60; Mismatches 144; Indels 60; Gaps 15;

QY 10 NTTSEKGNVAVGG---VLFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 66
DB 16 NQSSAADGCGSVSVAPFIMTMTVTFVGNALMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKLLSPVLAAYQNRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
DB 71 WLALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCCTFFGLTMTVFGSLSLVASAM 128

QY 127 ALECWLSLGHPPFFRHHITRLGALVAPV---VSASFSLAFALPFGMGKGFVQVCPGTWTC 183
DB 129 AVERALAIRAPHWYASHMKTR-----ATFVLLGVWLSVLAFLPVLGVRYSVQWPGTWC 184

QY 184 FI-----QMVHEGSLSVLGVSYSLLMALLVLATVLCNLGAMRNLYAMHRRRLQR 234

```

Db      185 FISTGPAGNETDSAREPGSVA---FASAFACLGGLLALVVTTFACNLATIKALVS----- 234
Qy      235 HPRSCTRDCAEPRAD---GREASQPLELDHLLALLMTVLTMCSLPVIYRAYYGAFK 291
Db      235 ---RCRAKAAASQSSAQWGRITTETAIQ-----LMGIMCVL-SVCWSPLLIWMLKMFN 284
Qy      292 DVKE---KNRTSEAE---DLRALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLRY 345
Db      285 QMSVEQCKTQMGKEKCNFLIAVRLASLNQILDPPWYLLLRKILLRKFQ---IRD--H 339
Qy      346 RSRCSNSTNM 355
Db      340 TNYASSTSL 349

```

Search completed: April 22, 2005, 21:30:02
 Job time : 17.5389 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 18:00:17 ; Search time 63.5786 Seconds
(without alignments)
2891.482 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFYRCQNTVSEKGNLSA.....IRPLRYRSCSNSTNMESL 359

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1864	100.0	359	1 P22R_HUMAN	Q13258 homo sapien
2	1388.5	74.5	357	2 O9R261	Q9R261 rattus norv
3	1386.5	74.4	357	2 O35932	O35932 rattus norv
4	1347.5	72.3	357	1 P22R_MOUSE	P70263 rattus norv
5	1342.5	72.0	357	2 O8CQK3	O8CQK3 mus musculu
6	714	38.3	361	1 P222_CANFA	O9XCH2 canis famli
7	707.5	38.0	362	1 P222_MOUSE	O62053 mus musculu
8	688	36.9	358	1 P222_HUMAN	P43116 homo sapien
9	674	36.2	357	1 P222_RAT	O62928 rattus norv
10	665	35.7	361	2 O8H157	O8H157 oryctolagus
11	662	35.5	352	2 O8M009	O8M009 bos taurus
12	658.5	35.3	371	2 O6N215	O6N215 xenopus lae
13	628.5	33.7	385	1 P12R_BOVIN	P79393 bos taurus
14	597	32.0	386	1 P12R_HUMAN	P43119 homo sapien
15	592.5	32.0	415	1 P12R_MOUSE	P43252 mus musculu
16	592.5	31.8	308	2 O8B275	O8B275 mus musculu
17	585.5	31.4	416	1 P12R_RAT	P43253 rattus norv
18	497.5	26.7	281	2 O6PFT8	O6PFT8 brachydanio
19	458.5	24.6	488	2 O91VE4	O91VE4 mus musculu
20	458.5	24.6	513	1 P224_MOUSE	P33240 mus musculu
21	452.5	24.3	488	1 P224_RAT	P43114 rattus norv
22	446.5	24.0	492	2 O8M008	O8M008 bos taurus
23	445	23.9	492	2 O9T016	O9T016 canis famli
24	443	23.8	488	1 P224_HUMAN	P35408 homo sapien
25	442	23.7	490	2 O95J39	O95J39 macaca fasc
26	442	23.7	490	2 O7JGJ7	O7JGJ7 papio hamad
27	440	23.6	490	1 P224_PANTR	O95K7C pan troglod
28	436.5	23.4	488	1 P224_RABIT	O28691 oryctolagus
29	393	21.1	292	2 O7TSX4	O7TSX4 rattus norv
30	316.5	17.0	154	2 O7TSX3	O7TSX3 mus musculu
31	312	16.7	362	2 O6PDE2	O6PDE2 mus musculu

32	310	16.6	360	2 O99PG3	O99PG3 rattus norv
33	308	16.5	365	1 P223_MOUSE	P30557 mus musculu
34	308	16.5	365	1 P223_RAT	P34980 rattus norv
35	302.5	16.2	416	2 O6VPS5	O6VPS5 canis famli
36	300.5	16.1	168	2 O95M50	O95M50 bos taurus
37	300.5	16.1	370	2 O6VPS4	O6VPS4 canis famli
38	297.5	16.0	390	1 P223_HUMAN	P43115 homo sapien
39	296.5	15.9	411	1 P223_RABIT	P46069 oryctolagus
40	292.5	15.7	369	1 P223_HUMAN	P21731 homo sapien
41	292.5	15.7	407	2 O75278	O75278 homo sapien
42	291.5	15.6	366	2 O6TTM3	O6TTM3 homo sapien
43	291.5	15.6	393	2 O00326	O00326 homo sapien
44	291.5	15.6	402	2 O00325	O00325 homo sapien
45	284.5	15.3	417	1 P223_BOVIN	P34979 bos taurus

ALIGNMENTS

RESULT 1
PD2R_HUMAN STANDARD, PRT, 359 AA.
ID PD2R_HUMAN Q13258; Q13250; Q13251.
AC Q13258; Q13250; Q13251.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
GN Name=PTGDR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=55370201; PubMed=7642548; DOI=10.1074/jbc.270.32.18910;
RA Bote Y., Sawyer N., Stipez D.M., Metters K.M., Abramovitz M.;
RT "Molecular cloning and characterization of the human prostanoid DP
receptor.";
RL J. Biol. Chem. 270:18910-18916(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toibiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
-1- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
this receptor is mainly mediated by G(s) proteins that stimulate
adenylate cyclase, resulting in an elevation of intracellular
cAMP. A mobilization of calcium is also observed, but without
formation of inositol 1,4,5-trisphosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in retina and small intestine.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC modified and this statement is not removed. Usage by and for commercial
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DR EMBL; U31332; AAC50178.1; -;
 DR EMBL; U31098; AAC50176.1; -;
 DR EMBL; U31099; AAC50177.1; -;
 DR EMBL; BC040968; AAC40968.1; -;
 DR PIR; I39153; I39153.
 DR Genew; HGNC:9591; PTGDR.
 DR MIM; 604687; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004956; F:prostaglandin D receptor activity; NAS.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; NAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000376; Glnndn_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1788; PROSTANOIDR.
 DR PRINTS; PRO0429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; FALSE_NEG.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 21
 FT TRANSSEM 22 42
 FT TRANSSEM 43 59
 FT TRANSSEM 60 80
 FT TRANSSEM 81 107
 FT TRANSSEM 108 128
 FT TRANSSEM 129 150
 FT TRANSSEM 151 171
 FT TRANSSEM 172 195
 FT TRANSSEM 196 216
 FT TRANSSEM 217 262
 FT TRANSSEM 263 283
 FT DOMAIN 284 310
 FT TRANSSEM 311 331
 FT TRANSSEM 332 359
 FT DISULFID 105 183
 FT CARBOHYD 10 10
 FT CARBOHYD 90 90
 FT CARBOHYD 297 297
 SQ SEQUENCE 359 AA; 40270 MW; 098F89F38D0BE12A CRC64;

Query Match 100.0%; Score 1864; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 4.1e-137;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPSPV 60
 DB 1 MKSPFYRCNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPSPV 60
 QY 61 FYMVGCTVTDLLGKCLSPVLAAYVQNRSLRVLPALDNLCOAFAPFMSFGSLST 120
 DB 61 FYMVGCTVTDLLGKCLSPVLAAYVQNRSLRVLPALDNLCOAFAPFMSFGSLST 120
 QY 121 LQILAMLECWLSLGHFFRYRHTLRIGALVAPVSAFSLAFCLPFWGFGKFOYCPG 180
 DB 121 LQILAMLECWLSLGHFFRYRHTLRIGALVAPVSAFSLAFCLPFWGFGKFOYCPG 180
 QY 181 TWCFIQWHEBGSLSVLGYSSLMALVLAIVLCNIGAMRNLYAMHRRLOQRHPSCT 240
 DB 181 TWCFIQWHEBGSLSVLGYSSLMALVLAIVLCNIGAMRNLYAMHRRLOQRHPSCT 240
 QY 241 RDCAEPADGREGAPQPLEEDHLLALLMTVLFMCSLPVYRAYYGAFCQVKEKRTS 300
 DB 241 RDCAEPADGREGAPQPLEEDHLLALLMTVLFMCSLPVYRAYYGAFCQVKEKRTS 300
 QY 301 EEAEDLRALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLAYRSRCSNSTMESSL 359

DB 301 EEAEDLRALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLAYRSRCSNSTMESSL 359

RESULT 2

Q9R261 ID Q9R261 PRELIMINARY; PRT; 357 AA.

AC Q9R261;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Prostaglandin D2 receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STEAIN=Sprague-Dawley;
 RX MEDLINE=99376163; PubMed=10448933; DOI=10.1016/S0014-2999(99)00358-1;
 RA Wright D.H., Nantel F., Metters K.M., Ford-Hutchinson A.W.;
 RT "A novel biological role for prostaglandin D2 is suggested by
 RT distribution studies of the rat Dp prostanoid receptor.";
 RL Eur. J. Pharmacol. 377:101-115 (1999).

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004956; F:prostaglandin D receptor activity; IEA.
 DR GO; GO:0004972; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:chromoblastane receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000376; Glnndn_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1788; PROSTANOIDR.
 DR PRINTS; PRO0854; PRSTNOIDPR.
 DR PRINTS; PRO0429; THROMBOXANR.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KM Receptor.
 SQ SEQUENCE 357 AA; 39768 MW; A65E1355E52E8286 CRC64;

Query Match 74.5%; Score 1388.5; DB 2; Length 357;
 Best Local Similarity 76.1%; Pred. No. 4.4e-100;
 Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;

QY 6 YRCQNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPSPVFMV 65
 DB 5 YRCQNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPSPVFMV 64
 QY 66 CGLTVTDLLGKCLSPVLAAYVQNRSLRVLPALDNLCOAFAPFMSFGSLSTLOLLA 125
 DB 65 CGLTVTDLLGKCLSPVLAAYVQNRSLRVLPALDNLCOAFAPFMSFGSLSTLOLLA 124
 QY 126 MALECWLSLGHFFRYRHTLRIGALVAPVSAFSLAFCLPFWGFGKFOYCPGTCFI 185
 DB 125 MALECWLSLGHFFRYRHTLRIGALVAPVSAFSLAFCLPFWGFGKFOYCPGTCFI 184
 QY 186 QWHEBGSLSVLGYSSLMALVLAIVLCNIGAMRNLYAMHRRLOQRHPSCTPCA 245
 DB 185 QWHEBGSLSVLGYSSLMALVLAIVLCNIGAMRNLYAMHRRLOQRHPSCTPCA 244
 QY 246 PRADGREGAPQPLEEDHLLALLMTVLFMCSLPVYRAYYGAFCQVKEKRTSEAD 305
 DB 245 SGSDYRGSNPPLEEDHLLALLMTVLFMCSLPVYRAYYGAFCQVKEKRTSEAD 301
 QY 306 LRALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLAYRSRCSNSTMESSL 359
 DB 302 LQALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLAYRSRCSNSTMESSL 357

RESULT 3

035932 ID 035932 PRELIMINARY; PRT; 357 AA.
 AC 035932;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Prostoglandin D2 receptor.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX MEDLINE=98387174; PubMed=9721719;
 RA Geraschenko D., Beuckmann C.T., Kanaoka Y., Eguchi N., Gordon W.C., Urade Y., Baan N.G., Hayashi O.,
 RT "Dominant expression of rat prostanoilid D2 receptor mRNA in leptomeninges, inner segments of photoreceptor cells, iris epithelium, and ciliary processes.";
 RL J. Neurochem. 71:937-945(1998).
 DR EMBL: U92289; AAB71762.1; -
 DR GO: GO:0016021; C: integral to membrane, IEA.
 DR GO: GO:0004956; F: prostaglandin D receptor activity, IEA.
 DR GO: GO:0004872; F: receptor activity, IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity, IEA.
 DR GO: GO:0004960; F: rhodopsin-like receptor activity, IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR000376; Gplndnd_receptor.
 DR InterPro: IPR008365; Prostanoidrecept.
 DR InterPro: IPR001105; Thbox_receptor.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PRO1788; PROSTANOIDR.
 DR PRINTS: PRO0854; PROSTNOIDPR.
 DR PROSITE: PRO0429; THROMBOXANR.
 DR PROSITE: PSS0262; G_PROTEIN_RECPT_F1_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 357 AA; 39802 MW; DB966276DD68184C CRC64;
 Query Match 74.4%; Score 1386.5; DB 2; Length 357;
 Best Local Similarity 76.1%; Pred. No. 6,3e-100;
 Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;
 QY 6 YRCQNTSVKSGKSAVWGVLFTSGILGNLALGLARSGKSGRRPLRLPLVDFVMV 65
 DB 5 YRCQAAWVERGSSATGVLFSGLGNLALVLLARSGSGCRPGPLPPPSVFLV 64
 QY 66 CGLTVDLLGKCLSPVLAAYQNRSLRYLAPALDNSLCOAFAPFMSFGLSTQLLA 125
 DB 65 CGLTIVHLGKCLSPVLAAYQNRSLKELRLPSGQLCEAPFLMSFGLSTQLLA 124
 QY 126 MALECMWLSLGHPPFYRRHITLRIGALVAPVSAFSLFALPFMGFGKPVQYCGTWCFT 185
 DB 125 MALECMWLSLGHPPFYRRHITLRIGALVAPVSAFSLFALPFMGFGKPVQYCGTWCFT 184
 QY 186 QMHEGSGSLVAGSVLYSSLMALVATVLCUGANRNIYARRLQRPSTRCAC 245
 DB 185 QMHHKRSFVSIVSVYSSLMALVATVLCUGANRNIYARRLQRPSTRCAC 244
 QY 246 PRADGSEASPOPEEDLHLLALMTVLFMTCSLPVYRAYVGAFOVKEKNTSEAD 305
 DB 245 SGSDYRHGSPNPEEDLHLLALMTVLFMTCSLPVYRAYVGAFOVKEKNTSEAD 301
 QY 306 LRLARFLSVISIVDPWFIIFRSVPFRIFFPKIFIRPLARYSRCSNS--TNMESL 359
 DB 302 LQALRFLSVISIVDPWFIIFRTSVFRMLFHKAFTRDLRYRNCSHSGWQTNMESTL 357

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostoglandin D2 receptor (Prostanoid D2 receptor) (PGD receptor).
 GN Name:Pgdr;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=95062232; PubMed=7972033;
 RA Hirata M., Kakizuka A., Aizawa M., Ushikubi F., Narumiya S.;
 RT "Molecular characterization of a mouse prostaglandin D2 receptor and functional expression of the cloned gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11192-11196(1994).
 CC -1- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of this receptor is mainly mediated by G(s) proteins that stimulate adenylylase cyclase, resulting in an elevation of intracellular cAMP. A mobilization of calcium is also observed, but without formation of inositol 1,4,5-trisphosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Most abundantly expressed in the ileum, followed by lung, stomach and uterus.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC EMBL: D29765; BAA06168.1; -
 CC EMBL: D29764; BAA06168.1; JOINED.
 DR MGD: MGI:102966; Pgdr.
 DR GO: GO:0004956; F: prostaglandin D receptor activity, IDA.
 DR GO: GO:0001785; F: prostaglandin J receptor activity, IDA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR000376; Gplndnd_receptor.
 DR InterPro: IPR008365; Prostanoidrecept.
 DR InterPro: IPR001105; Thbox_receptor.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PRO1788; PROSTANOIDR.
 DR PRINTS: PRO0429; THROMBOXANR.
 DR PROSITE: PSS0237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.
 DR PROSITE: PSS0262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 20
 FT TRANSMEM 21 41
 FT DOMAIN 42 58
 FT TRANSMEM 59 79
 FT DOMAIN 80 106
 FT TRANSMEM 107 127
 FT DOMAIN 128 149
 FT TRANSMEM 150 170
 FT DOMAIN 171 194
 FT TRANSMEM 195 215
 FT DOMAIN 216 261
 FT TRANSMEM 262 282
 FT DOMAIN 283 306
 FT TRANSMEM 307 327
 FT DOMAIN 328 357
 FT DISULFID 104 182
 FT CARBOHYD 2 2
 FT CARBOHYD 89 89
 SQ SEQUENCE 357 AA; 40005 MW; 91CBFFA75396B505 CRC64;
 Query Match 72.3%; Score 1347.5; DB 1; Length 357;
 Best Local Similarity 73.3%; Pred. No. 6.9e-97;
 Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;

```

QY 6 YRCNTTSVEKGNASVWGVLFSTGILGNLALGLARSGLGWCSRRRLPLPSVFYMLV
DB 5 YRCOTSTWVERGSATGTAVLFGAGLGNLALVILARSGLGSCRPPPLPPSVFVVLV
QY 66 CGLTVDLCKCLISPVVLAAYANRSLRYLAPALDNSLCOAFAPFMSFFGLSSTQLLA
DB 65 CGLTVDLCKCLISPVVLAAYANRSLRYLAPALDNSLCOAFAPFMSFFGLSSTQLLA
QY 126 MALECMWLSLGHPPFYRRHITLRGALVAPVVASASLAFCLPFGPKFQYCGTWCFL
DB 125 MAVECMWLSLGHPPFYRRHITLRGALVAPVVASASLAFCLPFGPKFQYCGTWCFL
QY 186 QMVEEGSLVIGSVYSSIMALLVATVLCNIGAMRNLYAMHRLQRRPSCTRDCAE
DB 185 QMVEEGSLVIGSVYSSIMALLVATVLCNIGAMRNLYAMHRLQRRPSCTRDCAE
QY 246 PRADGRASPOPLEEDHLLALMTVLFVTCSPVITYRAYGAFKDKVKNRTSEAD
DB 245 SGSDYRRGSLHPLEEDHLLALMTVLFVTCSPVITYRAYGAFKDKVKNRTSEAD
QY 306 LRALRFLSVISYDPMWIFIFRSVVERIFRPHKIFIRPLRVRSCNS--TMMESL 359
DB 302 LRALRFLSVISYDPMWIFIFRSVVERIFRPHKIFIRPLRVRSCNS--TMMESL 357

RESULT 5
08CCM3 PRELIMINARY; PRT; 357 AA.
ID 08CCM3
AC 08CCM3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430566C09 product:prostaglandin D receptor,
DE full insert sequence.
DE Name=Ptdgr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashinaga K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK032488; BAC27895.1; -.
DR MGI, MGI:102966; Ptdgr.
DR GO, GO:0016021; C:integral to membrane; TMS.
DR GO, GO:0004956; F:prostaglandin D receptor activity; IDA.
DR GO, GO:0001785; F:prostaglandin J receptor activity; IDA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000376; Glnadn_receptor.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR01786; PROSTANOIDR.
DR PRINTS: PR00854; PRSTNOIDPR.
DR PRINTS: PR00429; THROMBOXANR.
DR PROSITE, PS50262; G_PROTEIN_RECPT_P1_2, 1.
DR KMER.
SQ SEQUENCE 357 AA; 39990 MW; A0FAFE3E5D77E952 CRC64;
Query Match 72.0%; Score 1342.5; DB 2; Length 357;
Best Local Similarity 73.0%; Pred. No. 1.7e-96;
Matches 260; Conservative 39; Mismatches 52; Indels 5; Gaps 2;
QY 6 YRCNTTSVEKGNASVWGVLFSTGILGNLALGLARSGLGWCSRRRLPLPSVFYMLV
DB 5 YRCOTSTWVERGSATGTAVLFGAGLGNLALVILARSGLGSCRPPPLPPSVFVVLV
QY 66 CGLTVDLCKCLISPVVLAAYANRSLRYLAPALDNSLCOAFAPFMSFFGLSSTQLLA
DB 65 CGLTVDLCKCLISPVVLAAYANRSLRYLAPALDNSLCOAFAPFMSFFGLSSTQLLA
QY 126 MALECMWLSLGHPPFYRRHITLRGALVAPVVASASLAFCLPFGPKFQYCGTWCFL
DB 125 MAVECMWLSLGHPPFYRRHITLRGALVAPVVASASLAFCLPFGPKFQYCGTWCFL
QY 186 QMVEEGSLVIGSVYSSIMALLVATVLCNIGAMRNLYAMHRLQRRPSCTRDCAE
DB 185 QMVEEGSLVIGSVYSSIMALLVATVLCNIGAMRNLYAMHRLQRRPSCTRDCAE
QY 246 PRADGRASPOPLEEDHLLALMTVLFVTCSPVITYRAYGAFKDKVKNRTSEAD
DB 245 SGSDYRRGSLHPLEEDHLLALMTVLFVTCSPVITYRAYGAFKDKVKNRTSEAD
QY 306 LRALRFLSVISYDPMWIFIFRSVVERIFRPHKIFIRPLRVRSCNS--TMMESL 359
DB 302 LRALRFLSVISYDPMWIFIFRSVVERIFRPHKIFIRPLRVRSCNS--TMMESL 357

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RESULT 6
PE22_CANFA STANDARD; PRT; 361 AA.

AC 09XT82; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE receptor, EP2 subtype).
DE Name=PTGER2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99338573; PubMed=10410384; DOI=10.1016/S0090-6980(98)00081-1;
RA Hibbs T.A., Lu B., Smock S.L., Vestergaard P., Pan L.C., Owen T.A.;
RT "Molecular cloning and characterization of the canine prostaglandin E receptor EP2 subtype."
RL Prostaglandins Other Lipid Mediat. 57:133-147(1999).
CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of this receptor is mediated by G(s) proteins that stimulate adenylyate cyclase. The subsequent raise in intracellular cAMP is responsible for the relaxing effect of this receptor on smooth muscle (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC -----
CC EMBL: AF075602; AAD43140.1; -
DR InterPro: IPR001923; EP2_receptor.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR01105; Tbox_receptor.
DR Pfam: PF00001; Tcm.1; 1.
DR PRINTS: PRO0237; GPCRHOPODSN.
DR PRINTS: PRO1788; PROSTANOIDR.
DR PRINTS: PRO0581; PROSTOIDEPR2.
DR PRINTS: PRO0429; THROMBOXANR.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
KM G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 23 Extracellular (Potential).
FT TRANSSEM 24 47 1 (Potential).
FT DOMAIN 48 65 Cytoplasmic (Potential).
FT TRANSSEM 66 91 2 (Potential).
FT DOMAIN 92 111 Extracellular (Potential).
FT TRANSSEM 112 132 3 (Potential).
FT DOMAIN 133 151 Cytoplasmic (Potential).
FT TRANSSEM 152 176 4 (Potential).
FT DOMAIN 177 198 Extracellular (Potential).
FT TRANSSEM 199 223 5 (Potential).
FT DOMAIN 224 262 Cytoplasmic (Potential).
FT TRANSSEM 263 286 6 (Potential).
FT DOMAIN 287 299 Extracellular (Potential).
FT TRANSSEM 300 323 7 (Potential).
FT DOMAIN 324 361 Cytoplasmic (Potential).
FT DISULFID 109 187 By similarity.
FT CARBOHYD 6 6 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 361 AA; 40274 MW; BC997FC8BD4FBD4B CRC64;

Query Match 38.3%; Score 714; DB 1; Length 361;

Best Local Similarity 44.7%; Pred. No. 1.5e-47;
Matches 161; Conservative 54; Mismatches 115; Indels 30; Gaps 10;

QY 8 QNTTSVKGKSAWGVLFSTGLGNLALGLARSLGKMSRRPLRLP-SVYPMVC 66
DB 13 CESREWLPSGSPALSSAMFAGVIGNLIALALLRRRGGAGRGAGNSLSHVLVT 72
QY 67 GLTVTDLIGKCLSPVLAAYAKNSLRLVLPALDNSLCQAFAPFSPFGSLTQLAM 126
DB 73 ELVFTDLIGTCLISIVVLASARNGTMALEP--BRACCTYFAPMTFTSLATMLMFLAM 130
QY 127 ALECLSLGHPFPYRRHTLRLGALVAPVSAFSLAFCALPFGKFGVQCPGTWCFTQ 186
DB 131 ALERLYSLGRVPYGRHVRTRGGLAVPTIYTVSLFCSLPDILGQVQVQCPGTWCFTR 190
QY 187 MHEEGSLVLCGLSVLSSMLALVLTATVLCNLGAMRLYMRRLQHP-----RSCTR 241
DB 191 --HGR----YAVYQLVATLLLLIVAVLACNFSVYTLIMHRSRGRSCPSLGC-R 242
QY 242 DCAEPRADGRASPOPELEHLLHLLAMTVLFTMCSLPVYRAYGAFKDVKEKGRPSE 301
DB 243 DSGTRRGRGVVS--VAETHLLILAMITTPAICSLPFTTFAY-----MNEISS 291
QY 302 EAE--DLRALPLFVLSIVDPWIFIPSPVFRIFPKIFIR-PLVRSRCSNSTMESS 358
DB 292 RREKMDQLALRFLINSIIDPWFAIRPVLRLMRSLCCRVSLRAQDATQTSISQSN 351

RESULT 7
PE22_MOUSE STANDARD; PRT; 362 AA.

AC 062053; 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE receptor, EP2 subtype).
DE Name=PTGER2; Synonyms=Ptger2;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ddY; TISSUE=Lung;
RX MEDLINE=96000196; PubMed=7556658; DOI=10.1016/0014-5793(95)00966-D;
RA Katsuyama M., Nishigaki N., Sugimoto Y., Morimoto K., Negishi M.,
RA Narumiya S., Ichikawa A.;
RT "The mouse prostaglandin E receptor EP2 subtype: cloning, expression, and northern blot analysis."
RL PNAS Lett. 372:151-156(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toehiyuki S., Carninci P., Prange C.C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Roderfeldt Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 CC this receptor is mediated by G(s) proteins that stimulate
 CC adenylylate cyclase. The subsequent raise in intracellular cAMP is
 CC responsible for the relaxing effect of this receptor on smooth
 CC muscle.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D50589; BAA09137.1; -.
 DR EMBL; BC005440; AAH05440.1; -.
 DR PIR; S66674; S66674.
 DR MGI; MGI:97794; Ptger2.
 DR InterPro; IPR001923; EP2_receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHOPOSN.
 DR PRINTS; PRO1788; PROSTANOIDR.
 DR PRINTS; PRO0581; PRSTNOIDEP2R.
 DR PROSITE; PRO0429; THROMBOXANER.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 24
 FT TRANSSEM 25 48
 FT TRANSSEM 49 66
 FT TRANSSEM 67 92
 FT TRANSSEM 93 112
 FT TRANSSEM 113 133
 FT TRANSSEM 134 153
 FT TRANSSEM 153 177
 FT TRANSSEM 178 199
 FT TRANSSEM 200 224
 FT TRANSSEM 225 262
 FT TRANSSEM 263 286
 FT TRANSSEM 287 299
 FT TRANSSEM 300 323
 FT TRANSSEM 324 362
 FT DISULFID 110 188
 FT CARBOHYD 6
 SQ SEQUENCE 362 AA; 40478 MW; A79FCEB86771F44 CQC64;
 Query Match 38.0%; Score 707.5; DB 1; Length 362;
 Best Local Similarity 44.5%; Pred. No. 49e-47;
 Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;
 Oy 8 CONTTSVEKNSAWGVLFSTGLGNLALGLARSGLG--WCSRRRLPLPSVFWLV 65
 Db 14 CKSQWMLSGSPAISSWFSAGVLSNIALALARRRGRTGCSAGS-RTISLIFWLV 72
 Oy 66 CGLTVDLGLKCLSPVLAAYAQNRSRLVLAAPALDNLCOAFEFMSFFGLSSTLQLLA 125
 Db 73 TELVTDLGLTCLSPVLAAYSNQTLVLAAP--ESHACTYPAFTMTFFSLATMLMFA 130
 Oy 126 MALCEWLSLGHPPFRRIITRLGALVAPVVSASLSALCALPMGFGKFPVOCRTWCFI 185
 Db 131 MALRRYLSIGVPPFRRLSRGGALVAPVYGA SLFCSPLNLYGKVVYVOCRTWCFI 190
 Oy 186 OMVHEEGLSLVGLSVSSMALVLAIVTCNIGAMNLTAMRRRLORHRSCTRDCAE 245
 Db 191 R-HGR-----TAYIQVATMLLITVAIVACNISVIITLIRHRRSR--SRGLSGSS 241

Oy 246 PRADG--REASPOPLEDHLILALMTVLFMCSLPVTRYAYGAFKVKENRTSEE 302
 Db 242 LRQPSRRRERERTSMEEHTLILALIMITTFACSLPFIIFYMETSLSKER----- 295
 Oy 303 AEQRLARFLSVSYDVPWFIFFRSPVPRIFPHKIFIR-PLVRSRCSNSTWESS 358
 Db 296 -WDLARFLSVSYSDVPWFIFFRSPVPRIFPHKIFIR-PLVRSRCSNSTWESS 351
 RESULT 8
 PE22_HUMAN STANDARD; PRT; 358 AA.
 AC P43116;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
 DE receptor, EP2 subtype).
 GN Name=PTGER2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94359483; PubMed=8078484;
 RA Regan J.W., Bailey T.J., Pepperl D.J., Pierce K.L., Bogardus A.M.,
 RA Donnell J.E., Fairbairn C.E., Kedzie K.M., Woodward D.F., Gil D.W.;
 RT "Cloning of a novel human prostaglandin receptor with characteristics
 RT of the pharmacologically defined EP2 subtype.";
 RL Mol. Pharmacol. 46:213-220(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oakley C.J.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99453300; PubMed=10521663; DOI=10.1016/S0378-1119(99)00323-6;
 RA Smock S.L., Pan L.C., Castleberrry T.A., Lu B., Mather R.J., Owen T.A.;
 RT "Cloning, structural characterization, and chromosomal localization of
 RT the gene encoding the human prostaglandin E2 receptor EP2 subtype.";
 RL Gene 237:393-402(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 CC this receptor is mediated by G(s) proteins that stimulate
 CC adenylylate cyclase. The subsequent raise in intracellular cAMP is
 CC responsible for the relaxing effect of this receptor on smooth
 CC muscle.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Placenta and lung.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 CC EMBL; U19487; AAA61681.1; -.
 DR EMBL; X83868; CAA58749.1; -.
 DR EMBL; AF134202; AAD44177.1; -.
 DR EMBL; AF134201; AAD44177.1; JOINED.
 DR EMBL; AY275471; AAB32303.1; -.
 DR PIR; I38920; I38920.

DR PIR; S51312; S51312.
 DR Genew; HGNC:9594; PTGER2.
 DR MIM; 176804; -
 DR CO; GO:0005887; C:integral to plasma membrane; TAS.
 DR CO; GO:0004957; F:prostaglandin E receptor activity; TAS.
 DR CO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro; IPR001923; E22_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 23 Extracellular (Potential).
 FT TRANSSEM 24 47 1 (Potential).
 FT TRANSSEM 48 65 Cytoplasmic (Potential).
 FT DOMAIN 66 91 2 (Potential).
 FT TRANSSEM 92 111 Extracellular (Potential).
 FT TRANSSEM 112 132 3 (Potential).
 FT TRANSSEM 133 151 Cytoplasmic (Potential).
 FT TRANSSEM 152 176 4 (Potential).
 FT DOMAIN 177 198 Extracellular (Potential).
 FT TRANSSEM 199 223 5 (Potential).
 FT TRANSSEM 224 262 Cytoplasmic (Potential).
 FT TRANSSEM 263 299 6 (Potential).
 FT TRANSSEM 300 323 Extracellular (Potential).
 FT TRANSSEM 324 358 7 (Potential).
 FT DISUPFID 109 187 Cytoplasmic (Potential).
 FT CARBOHYD 3 3 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 6 6 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 96 96 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 287 287 N-linked (GlcNAc. . .) (Potential).
 FT CONFICT 150 150 R -> A (in Ref.1 and 3).
 SQ SEQUENCE 358 AA; 39760 MW; B3B0E2A3CFE2E363 CRC64;
 Query Match 36.9%; Score 688; DB 1; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.6e-45;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

AC Q62928;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
 DE receptor, EP2 subtype).
 GN Name=Ptger2;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=98103308; PubMed=9440134; DOI=10.1016/S0014-2999(97)00145-7;
 RA Nemoto K., Pilbeam C.C., Bilak S.R., Raetz L.G.;
 RT "Molecular cloning and expression of a rat prostaglandin E2 receptor
 of the EP2 subtype.";
 RL Prostaglandins 54:713-725(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, TISSUE=Spleen;
 RX MEDLINE=98141044; PubMed=9537820; DOI=10.1016/S0014-2999(97)01383-6;
 RA Bole Y., Stocco R., Sawyer N., Slipetz D.M., Ungtin M.D.,
 RA Neuschaefer-Rube F., Puschel G.P., Metters K.M., Abramovitz M.;
 RT "Molecular cloning and characterization of the four rat prostaglandin
 E2 prostanoid receptor subtypes.";
 RL Eur. J. Pharmacol. 340:227-241(1997).
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 this receptor is mediated by G(s) proteins that stimulate
 adenylyl cyclase. The subsequent raise in intracellular cAMP is
 responsible for the relaxing effect of this receptor on smooth
 muscle (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U48858; AAA97889.1; -
 DR EMBL; U94708; AAB53325.1; -
 DR RSD; 620020; Pcgert2.
 DR InterPro; IPR001923; EP2_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 24 Extracellular (Potential).
 FT TRANSSEM 25 48 1 (Potential).
 FT TRANSSEM 49 66 Cytoplasmic (Potential).
 FT TRANSSEM 67 92 Extracellular (Potential).
 FT TRANSSEM 93 112 2 (Potential).
 FT TRANSSEM 113 133 3 (Potential).
 FT TRANSSEM 134 152 Cytoplasmic (Potential).
 FT TRANSSEM 153 177 4 (Potential).
 FT TRANSSEM 178 199 Extracellular (Potential).
 FT TRANSSEM 200 224 5 (Potential).
 FT TRANSSEM 225 262 Cytoplasmic (Potential).
 FT TRANSSEM 263 286 Extracellular (Potential).
 FT TRANSSEM 287 299 Extracellular (Potential).
 FT TRANSSEM 300 323 7 (Potential).

FT DOMAIN 324 357 Cytoplasmic (Potential).
 FT DISUFID 110 188 By similarity.
 FT CARBOHYD 6 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 357 AA; 39771 MW; AAB22AE280AEFF80 CRC64;
 Query Match 36.2%; Score 674; DB 1; Length 357;
 Best Local Similarity 44.7%; Pred. No. 2e-44;
 Matches 148; Conservative 54; Mismatches 105; Indels 24; Gaps 8;
 QY 8 COUNTSVEKNSAVMGVLFSTGLGNLALGLARSGGLG--WGRRPRLPSPVFTMLV 65
 DB 14 CERSQVLLSDSPSISVFTAGVGLNMLALARRMRDPDTGSAGS-RTSISLFFHLV 72
 QY 66 GGLTVDLLGKCLISPVVLAAYAONRSLRVLPALDLSLCAFAFPMSPFGLSTLQLLA 125
 DB 73 TELVTDLLGCLISPVVLAAYASRNQTLVALP--ESRACVTFPMTFSLATMLMFLA 130
 QY 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAFPWGFQKPYQCGTWCFT 185
 DB 131 MALERYLAIGHPYRRYRRVSRGGLAVLPALVGSLLFCSLPILNYGEVYQCGTWCFT 190
 QY 186 QMHEBSLSVLGYSVYSSIMALLVATVLCNIGANRNLVAMHRLQHRPSTRCQAE 245
 DB 191 Q-HGR-----TAYLQYATVTLILLIYAVLGCNISVILNIRMQLRKR--SRGLSGSS 241
 QY 246 PRADG---REASPOQLBELDHLILALMTVLTWCSLPVITYRAYGAFKDKVKERTSEE 302
 DB 242 LRGGSSRRRGERTSMAETDHLILALMTITFVACSIPFTTFAIMDETSSKER----- 295
 QY 303 AEDLRALRFLSVISIVDPWIFIFRSPVFR 333
 DB 296 -WDLRALRFLSVNSIIDPWVFLIRPVLRL 325
 RESULT 10
 Q8HY57 PRELIMINARY; PRT; 361 AA.
 ID 08HY57
 AC 08HY57
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Prostaglandin E2 receptor EP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Breyer M.D.;
 RT "Cloning of rabbit prostaglandin E2 receptor EP2."
 RL J. Am. Soc. Nephrol. 7:1646-1646(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=12097143; DOI=10.1186/1471-2210-2-14;
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Redha R., Breyer R.M., Breyer M.D.;
 RT "Cloning and expression of the rabbit prostaglandin EP2 receptor."
 RL BMC Pharmacol. 2:14-14(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AY166779; AAO13013.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro: IPR001923; EP2_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR008365; Prostanoidrecept.
 DR InterPro: IPR001105; Thbox_receptor.
 Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTOIDEPR2.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW SEQUENCE 361 AA; 39945 MW; E735BC61F60B19D CRC64;
 Query Match 35.7%; Score 665; DB 2; Length 361;
 Best Local Similarity 42.6%; Pred. No. 1e-43;
 Matches 155; Conservative 50; Mismatches 117; Indels 42; Gaps 11;
 QY 8 COUNTSVEKNSAVMGVLFSTGLGNLALGLARSGGLGCSRRPLRPLP-SVFYMLVC 66
 DB 13 CERNQMLPSGESPAISVMSAGVLTGNLALALARRMRADAGRSAGRTSLFLFHLVLT 72
 QY 67 GLTVDLLGKCLISPVVLAAYAONRSLRVLPALDLSLCAFAFPMSPFGLSTLQLLA 126
 DB 73 ELVFTDLLGCLISPVVLAAYARNQTLVALP--DGRACVTFPAMTFSLATMLMFLA 130
 QY 127 ALSCWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAFPWGFQKPYQCGTWCFTQ 186
 DB 131 ALERYLSIGHPYRQCRITRRGLAVLPALVTSLLFCSLPILDYGERYQCGTWCFTIR 190
 QY 187 MHEBSLSVLGYSVYSSIMALLVATVLCNIGANRNLVAMHRLQHRPSTRCQAE 246
 DB 191 -HGR-----TAYLQYATVTLILLIYAVLGCNISVILNIRMQLRKR--SRGSPS 237
 QY 247 RADGREASP-----QPLELDHLILALMTVLTWCSLPVITYRAYGAFKDKVKERN 297
 DB 238 SGSGR-GGPTRRRGRGVSVAEETDHLILALMTITFVACSIPFTTFAIMDETSSKER--MN 287
 QY 298 RTSEBAE--DLRALRFLSVISIVDPWIFIFRSPVFRIFRKFIR-PLR---YRSRCS 350
 DB 288 ETSRREKMDLRLRFLSVNSIIDPWVFLIRPVLRLKMSVLCRVSRLTQATQTSCS 347
 QY 351 NSTN 354
 DB 348 TQSN 351
 RESULT 11
 Q8MJ09 PRELIMINARY; PRT; 352 AA.
 ID 08MJ09
 AC 08MJ09
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE EP2 receptor.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22694625; PubMed=12810564; DOI=10.1210/en.2002-0088;
 RA Arosh J.A., Bann S.K., Chapdelaine P., Emond V., Kim J.J.,
 RA MacLaren L.A., Fortier M.A.;
 RT "Molecular Cloning and Characterization of Bovine Prostaglandin E(2)
 RT Receptor EP2 and EP4: Expression and Regulation in Endometrium and
 RT Myometrium during the Estrous Cycle and Early Pregnancy."
 RL Endocrinology 144:3076-3091(2003).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AF539402; AA001234.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro: IPR001923; EP2_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR008365; Prostanoidrecept.
 DR Pfam: PF00001; 7cm_1, 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PRINTS: PR01788; PROSTANOIDS.
 DR PRINTS: PR00581; PROSTANOIDE2R.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 KW SEQUENCE 352 AA; 39726 MW; 9EB8FB445B37287 CRC64;

Query Match 35.5%; Score 662; DB 2; Length 352;
 Best Local Similarity 42.7%; Pred. No. 1,76-43;
 Matches 149; Conservative 59; Mismatches 115; Indels 26; Gaps 8

QY 17 GNSAVMGVLPSTGILLGNLLAIGLARSGLGWCSRRPLRPPLP-SYFYMVCGLTVTDLIG 75
 DB 22 GESPAISSVMETAGVLGNLLALVRRMRGDSGRSGSKNSISLFFHLYLVTELVTDLIG 81
 QY 76 KCLLSPPVLLAAYQNRSLRVLAPALDNLCOAFAPFSGFLSGSTLQLLAMALBCWSLG 135
 DB 82 TCLLSPPVLLAAYQNRSLRVLAPALDNLCOAFAPFSGFLSGSTLQLLAMALBCWSLG 139
 QY 136 HPEFRRIITRLGALVAPVVSAPSLARCALPFWGKGFVQCPGTQCFIQVHEGSL 195
 DB 140 HPYRQKRVTRSGALVAPVPTIYISLFCSPLELHMKTAQNPETWCFIG--HKQT-- 195
 QY 196 VLGYSVLYSSIMALLVLTATVLCNIGAMENLYAMHRLQRHPSCTRDCAEPADGREASP 255
 DB 196 ---YLRLVATLLILLIIIVLACNPFSEVINLILHMRGRGRSNGPGLSGSHRAERVSNA- 251
 QY 256 QPLELDELHLLALMTVLFPTMCSLPVITYRAYGAFKDYKEKNRTSSEADILPAIRFLSVI 315
 DB 252 ---BETHDLILALMTITITFAVCSLPTITFAV-----MNRSSSKEXKMDLQALRFLISN 301
 QY 316 SIYVPWPIIFIRSPVPIEFPHKIFIR-PLR-----YRSCNSTWNESL 359
 DB 302 SIIDPMVPAIRLPVLRMSRVLCRVSILRTOEATOTISCTQSNASKOI 350

RESULT 12

Q6NZ15 PRELIMINARY; PRT; 371 AA.

AC Q6NZ15;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE MGC69060 Protein.
 GN Name=MGC69060;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=32388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shellen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.T.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Ayman R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodríguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shchepenko Y., Bouffard G.G.,
 RA Blakeley A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.U., Marra M.A.; analysis of more than 15,000 full-length human
RT "Generation and Initial Analysis of Sequences." ;
RT and mouse cDNA sequences." ;
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/adv.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative." ;
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC066120; AAF66120.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004957; F: prostaglandin E receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0004960; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaling. . ; IEA.
DR InterPro: IPR001923; E2E receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR008365; ProstanoidRecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam; Pf00001; 7tm_1; 1.
DR PRINTS; PR002337; GPCR_RHODOPSIN.
DR PRINTS; PR01788; PROSTANOIDR.
DR PRINTS; PR00581; PRSTNOIDEP2.
DR PRINTS; PR00429; THROMBOXANR.
DR PROSITE; PSS0262; G_PROTEIN_RECPT_P1_2; 1.
SQ SEQUENCE 371 AA; 41896 MW; 76B83A03B5E5B0AD CRC64;

Query Match	35.3%	Score 658.5	DB 2	Length 371
Best Local Similarity	39.5%	Pred. No. 3.3e-43		
Matches 141	Conservative 71	Mismatches 110	Indels 35	Gaps 9

Query	8	CONTTSVEKGNASAVMGVLFESTGLIGNLALGELLARSGLCGMSRRPLRPLPSVFMYLVCG	67
Ds	9	CESNCCHNCGSSPAVSAVMFSAVLGNLNLVLLEN-----RRRAVAGTMSLPHILVTG	62
Qy	68	LTVTDLIGKCLLSPVTLAATAQNSFLKVLAPALNLSLCOAFAPFMSFFGLSSTLOLMA	127
Ds	63	LVIYDLMGTCMISPVVLASYSNLTLLTAGSDRIRVCYYFAFMFTPSLATMTLVLFPAMA	122
Qy	128	LEGLSLGHPPEFYRRHITLRLGALVAVPVSAFSLAFCALPFGMGKFPVQYCGTWCFTOM	187
Ds	123	LERMAALGHPIVYEKFLSKCGGLTVPVIYSFCLFCLLPMNGGEYIYQYCGTWCFTIM	182
Qy	188	--VAHEGSLVLTGYSVLYSSIMALLVATVLCNLGAMKNTLYAMHRLOLRHRSCTRDCAE	245
Ds	183	RGCHINSGTNI-VSTLYATLTLTLTLIAVLTCNFTIVSLVRMKR-QKARLVTK----	236
Qy	246	PRADGRASPOPLEEDLHLLMLAMTVLFTWCSPVITYRAYGAFKDYKKNRISSEED	305
Ds	237	-----RERMMS--BEIDHLLLSMTIIFLFCSPVAQVYMNRFSPDRNDK-----RD	285
Qy	306	LRAALRFYSVSIYDVPFIIFRSPVPRIFPKPII-RPLRYR-----SRCGNS	352
Ds	286	LIALRFISVNSIIDPVYFVLRPSVLAIRIVLCCQPKFKIKELAKSPSLTSRLSNT	342

RESULT 13	P12R BOVIN	STANDARD;	PRT;	385 AA.
AC	P79393;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			

DE Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
 DE (Prostaglandin I2 receptor).
 GN Name=PTGIR;
 OS Bos taurus (Bovine).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hasse A., Schroer K.;
 RT "Cloning and sequencing of the bovine prostacyclin receptor gene,"
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGI2).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z93039; CAB07510.1; -;
 DR EMBL; Z93040; CAB07510.1; JOINED.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000370; IP_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1786; PROSTANOIR.
 DR PRINTS; PRO0429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KM Transmembrane.
 FT DOMAIN 1 16 Extracellular (Potential).
 FT TRANSSEM 17 38 1 (Potential).
 FT DOMAIN 39 51 Cytoplasmic (Potential).
 FT TRANSSEM 52 76 2 (Potential).
 FT DOMAIN 77 94 Extracellular (Potential).
 FT TRANSSEM 95 115 3 (Potential).
 FT DOMAIN 116 134 Cytoplasmic (Potential).
 FT TRANSSEM 135 158 4 (Potential).
 FT DOMAIN 159 181 Extracellular (Potential).
 FT TRANSSEM 182 208 5 (Potential).
 FT DOMAIN 209 234 Cytoplasmic (Potential).
 FT TRANSSEM 235 259 6 (Potential).
 FT DOMAIN 260 273 Extracellular (Potential).
 FT TRANSSEM 274 294 7 (Potential).
 FT DOMAIN 295 385 Cytoplasmic (Potential).
 FT DISULFID 5 165 By similarity.
 FT DISULFID 92 170 By similarity.
 FT LIPID 308 308 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 7 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 385 AA; 41247 MW; 0CDAS44D18E035C7 CRC64;
 Query Match 33.7%; Score 628.5; DB 1; Length 385;
 Best Local Similarity 44.1%; Pred. No. 7.4e-41;
 Matches 156; Conservative 46; Mismatches 109; Indels 43; Gaps 11;
 QY 8 CONTSVKGNKSAVMGVLFSTGLLNLGLIARSLGKCSRRLPLPSVFTMLVCG 67
 DB 5 CRNLTIVRDSVGPATSTLTFVAGVNGALGIILG-----ARRHSR--PSAFVAVLTG 55
 QY 68 LITVDLIGKLLSVTLAAVYQNSRLRTA---PALDNLSCQAFAPFSPFGSSLTQL 124
 DB 56 LGVTDLIGTCPLSPAVFAVYARNSSLGLAAGRA---LCDARAFAPFATFPGLASTILF 111

QY 125 AMALBECMLSGHPFFTRRHTTLRLGLVAVVSAFSLACALPMPGPKGVOCPTGTCF 184
 DB 112 AMAVERCIALSHPYLVAQLDGPERRARIALPAIYAFCTIFCSLPFLIGHQGYCPGSMCF 171
 QY 185 IOM-VHEBGLSVLYGSVYSSIMALLVATVLCNIGAMENILYAMRRRLORHRSCTPDC 243
 DB 172 IRRRSABPGGCAPL---LAVSLVALLVAIYLCNSVTLSLRMTROQRHQRARCP-- 226
 QY 244 AEPKADGREASPOPLELDHLLIALLMTVLTFTWCSLPVI--YRAYYGAFDVKRKNRTSE 301
 DB 227 --PRAGS-----DEVHLLIALLMTGIMAVCSPLTFQIRGFQALAP-----DSG 270
 QY 302 EADDLARLRFLSYISYIDPFITFRSPV--RIFPHKIFTRPLRYRSCNS 352
 DB 271 EMDLILAFRENAENPILDPVFIIFRKSVPRLKMLFCCLYSRPAQGSRTSLIS 324
 RESULT 14
 ID P12R_HUMAN STANDARD; PRT; 386 AA.
 AC P43119;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
 GN Name=PTGIR; Synonyms=PRIPR;
 OS Homo sapiens (Human).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94216334; PubMed=7512962;
 RA Bole Y., Rushmore T.H., Darmon-Goodwin A., Grygorczyk R.,
 RA Slipeiz D.M., Metters K.M., Abramovitz M.;
 RT "Cloning and expression of a cDNA for the human prostanoid IP
 RT receptor";
 RL J. Biol. Chem. 269:12173-12178 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94237286; PubMed=7514139; DOI=10.1016/0014-5793(94)00355-6;
 RA Katsuyama M., Sugimoto Y., Namba T., Irie A., Negishi M., Narumiya S.,
 RA Ichikawa A.;
 RT "Cloning and expression of a cDNA for the human prostacyclin
 RT receptor";
 RL FEBS Lett. 344:74-78 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=95008066; PubMed=7923647;
 RA Nakagawa O., Tanaka I., Ueui T., Harada M., Sasaki Y., Itoh H.,
 RA Yoshimasa T., Namba T., Narumiya S., Nakao K.;
 RT "Molecular cloning of human prostacyclin receptor cDNA and its gene
 RT expression in the cardiovascular system";
 RL Circulation 90:1643-1647 (1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95394450; PubMed=7665161;
 RA Ogawa Y., Tanaka I., Inoue M., Yoshitake Y., Isse N., Nakagawa O.,
 RA Ueui T., Itoh H., Yoshimasa T., Narumiya S.;
 RT "Structural organization and chromosomal assignment of the human
 RT prostacyclin receptor gene";
 RL Genomics 27:142-148 (1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP PALMITOYLATION.
 RX MEDLINE=22486644; PubMed=12488443; DOI=10.1074/jbc.M210637200;
 RA Miggin S.M., Lawler O.A., Kinsella B.T.;
 RT "Palmitoylation of the human prostacyclin receptor. Functional
 RL implications of palmitoylation and isoprenylation.";
 RL J. Biol. Chem. 278:6947-6958(2003).
 RN [7]
 RP DISULFIDE BONDS.
 RX PubMed=15194446; DOI=10.1016/j.ejphar.2004.04.041;
 RA Giguere V., Gallant M.A., de Bruin-Fernandes A.J., Parent J.-L.;
 RT "Role of extracellular cysteine residues in
 RT dimerization/oligomerization of the human prostacyclin receptor.";
 RL Eur. J. Pharmacol. 494:11-22(2004).
 CC -1- FUNCTION: Receptor for prostacyclin (prostacyclin I2 or PG12).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L29016; AAA36448.1; -;
 DR EMBL; D25418; BAA05008.1; -;
 DR EMBL; D25634; BAA06110.1; -;
 DR EMBL; D38127; BAA07325.1; -;
 DR EMBL; D38128; BAA07325.1; JOINED.
 DR EMBL; AY242134; AAO92301.1; -;
 DR PIR; A57066; A57066; PTGIR.
 DR Genew; HGNC:9602; PTGIR.
 DR MM; 600022; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004959; F:prostacyclin I2 receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007187; P:c-protein signaling, coupled to cyclic nucl. . .; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000370; IP_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR Pfam; PF000105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PSS0264; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Transmembrane.
 FT DOMAIN 1 16
 FT TRANSNM 17 38
 FT DOMAIN 39 51
 FT TRANSNM 52 76
 FT DOMAIN 77 94
 FT TRANSNM 95 115
 FT DOMAIN 116 134
 FT TRANSNM 135 158
 FT DOMAIN 159 181
 FT TRANSNM 182 208
 FT DOMAIN 209 235
 FT TRANSNM 236 260
 FT DOMAIN 261 274
 FT TRANSNM 275 295
 FT DOMAIN 296 311
 FT TRANSNM 312 333
 FT DISULFID 5 165
 FT DISULFID 92 170
 FT LIPID 308 308
 FT LIPID 311 311
 FT CARBOHYD 7 7
 SQ SEQUENCE 386 AA; 40955 MW; 2B6B0CDBACE1608 CRC64;

Query Match 32.0%; Score 597; DB 1; Length 386;
 Best Local Similarity 42.3%; Pred. No. 2,1e-38;
 Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;
 QY 8 CONTSVKGNKSAVWGVLFSTGLGNLALGLIARSGIWCGRRLPRLPSVFMVLCG 67
 DB CRNLTYVRSVGVPATSLTFMFAVGAVGNGALGILS-----ARRPAR--PSAPAVLVTG 55
 QY 68 LTVYDILGKLLSVVLAARQNRSLFVA---PALNSICQAFAPFMSFGLSSTYQL 124
 DB 56 LAATDILGTSFLSPAVVAARNSLGLARGPA---LCDAPAFMTTFGLASMLILF 111
 QY 125 AMALECWLISGHPFFYRHTLRGALVAVVSAFSLAFCLAPMGSGKFGVYCPGTWCF 184
 DB 112 AMAVERTLASHPLVYQDQDPRCARLALPAIYAFVLPALPLGLGQHQYCPGSMCF 171
 QY 185 IQM--VHEGSLSVLGYSVLSIMALLVATVLCNIGAMRNLYAMRRLQRHRSCTRD 242
 DB 172 LRMRWAPGGA---AFSLAVAGLVALLVAIFLCNGSVTLISCRMYRQGRHGS---- 223
 QY 243 CAERADGRASQPL---EEDHLLALMTVLFVTCSPVYIYRAYGAFKDYKERT 299
 DB 224 -----LGRPRPTGEVDHLILALMTVMVAVCSLPITRFTQAVAP-----DS 268
 QY 300 SEAEDELALRFLSVISIVDPWIFIPRSPVFR 332
 DB 269 SSEMDLAFRFYAFNPILDPWFILFRKAVPQ 301
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 ID P12R MOUSE
 AC P43252;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 25-JAN-2005 (Rel. 46, last annotation update)
 DE Prostacyclin receptor (Prostanoid IP receptor). (PGI receptor)
 DE (Prostaglandin I2 receptor).
 GN Name=Ptgir;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94193694; PubMed=7511597;
 RA Namba T., Oida H., Sugimoto Y., Negishi M., Kakizuka A., Ichikawa A.,
 RA Narumiya S.;
 RT "cDNA cloning of a mouse prostacyclin receptor. Multiple signaling
 RT pathways and expression in thymic medulla.";
 RL J. Biol. Chem. 269:9986-9992(1994).
 CC -1- FUNCTION: Receptor for prostacyclin (prostacyclin I2 or PG12).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D26157; BAA05144.1; ALT_INIT.
 DR MGD; MGI:99535; Ptgir.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000370; IP_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR RHODOPSIN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1;
 DR PROSITE; PS50262; G_PROTEIN_RECP_F2_1;
 DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Transmembrane.
 FT DOMAIN 1 44 Extracellular (Potential).
 FT TRANSMEM 45 66 1 (Potential).
 FT DOMAIN 67 79 Cytoplasmic (Potential).
 FT TRANSMEM 80 104 2 (Potential).
 FT DOMAIN 105 122 Extracellular (Potential).
 FT TRANSMEM 123 143 3 (Potential).
 FT DOMAIN 144 162 Cytoplasmic (Potential).
 FT TRANSMEM 163 186 4 (Potential).
 FT DOMAIN 187 215 Extracellular (Potential).
 FT TRANSMEM 216 236 5 (Potential).
 FT DOMAIN 237 263 Cytoplasmic (Potential).
 FT TRANSMEM 264 288 6 (Potential).
 FT DOMAIN 289 301 Extracellular (Potential).
 FT TRANSMEM 302 322 7 (Potential).
 FT DOMAIN 323 415 Cytoplasmic (Potential).
 FT DISULFID 33 193 By similarity.
 FT DISULFID 120 198 By similarity.
 FT LIPID 335 335 S-palmitoyl cysteine (By similarity).
 FT LIPID 338 338 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 415 AA; 44462 MW; 306929582DDDD24C CRC64;

Query Match 32.0%; Score 596.5; DB 1; Length 415;

Best Local Similarity 42.8%; Pred. No. 2.5e-38;
 Matches 139; Conservative 43; Mismatches 114; Indels 29; Gaps 7;

QY 8 COUNTSVKNSAVMGVLTSTGLGNLALGLARSGLCSSRRPLRPLPSVFMVCG 67
 DB 33 CWNITTVQDSVGPATSTLMFVAGVNGLAGILG-----ARR--RSHPSAPAVLVGT 83
 QY 68 LTVTDLIGKCLISPVLAAYVQNRSLRYLAPALDNSLCOAFPMSPFGLSSTLQLAMA 127
 DB 84 LAVTDLIGTCLTSPAVFAVARNSSILGLAHG-GTMLCDTFAPAMTFGLASTLILFAMA 142
 QY 128 LECWLSLGHPPFFRRHITLRLGALVAPVSAFSLAFQALPFWGKGVQYCGTWCTIQM 187
 DB 143 VERCLALSHPLYAQLDGPRCARPALPSIYAFCCIFCSLPLGLGEHQOYCPGSMCFIRM 202
 QY 188 VHEGSLSLVGYSLVSSIMALLVLAIVLCSLGMARNLYAMHRLQHPHSCTRDCAEP 247
 DB 203 --RSAQPGGCAFSLAIVASLMLVTSIFPCNGSVTSLYHMYRQQRHSGSFV-----PT 255
 QY 248 ADGREASPOPLEEDHLILLALMTVLFTMCSLPVIYRAYYGAFKDVKEKNTSEADLR 307
 DB 256 SRARE-----DEVYHLLILALMTVIMAVCSLPLMIRGFTQAIAP-----DSREMGDL 303
 QY 308 ALRFLSVISIVDPWIFIIIRSPVFR 332
 DB 304 AFRENAFNPIIDPWVFILFRKAVFQ 328

Search completed: April 22, 2005, 21:29:25
 Job time : 64.5786 secs

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OM protein - protein search, using SW model

Run on: April 22, 2005, 21:29:33 ; Search time 186.351 Seconds
(without alignments)
641.112 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MMSPFYRCNTTSVEKNSA.....IRPLRYRSCSNSTNMESL 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1864	100.0	359	14	US-10-225-567A-287 Sequence 287, App
2	1864	100.0	359	15	US-10-225-567A-2370 Sequence 2370, App
3	689	37.0	358	14	US-10-352-684A-291 Sequence 291, App
4	689	37.0	358	15	US-10-352-684A-36 Sequence 36, App1
5	689	37.0	358	15	US-10-366-288-36 Sequence 36, App1
6	689	37.0	358	15	US-10-755-889-92 Sequence 92, App1
7	688	36.9	358	13	US-10-108-714-4 Sequence 4, App1
8	688	36.9	358	17	US-10-684-206-38 Sequence 38, App1
9	683	36.6	358	17	US-09-825-509-559 Sequence 559, App
10	683	36.6	358	17	US-10-925-095-559 Sequence 559, App
11	597	32.0	386	14	US-10-225-567A-285 Sequence 285, App
12	518.5	27.8	289	15	US-10-108-260A-3907 Sequence 3907, App
13	443	23.8	488	14	US-10-225-567A-296 Sequence 296, App

14	443	23.8	488	14	US-10-320-351-3 Sequence 3, App1
15	443	23.8	488	15	US-10-295-027-1326 Sequence 1326, App
16	443	23.8	488	15	US-10-755-889-1370 Sequence 1370, App
17	442	23.7	480	14	US-10-243-501-3 Sequence 3, App1
18	440	23.6	488	10	US-09-826-509-561 Sequence 561, App
19	440	23.6	488	17	US-10-925-095-561 Sequence 561, App
20	440	23.6	490	14	US-10-243-351-2 Sequence 2, App1
21	298.5	16.0	393	14	US-10-060-902-28 Sequence 28, App1
22	298.5	16.0	393	15	US-10-354-247-28 Sequence 28, App1
23	297.5	16.0	390	14	US-10-060-902-22 Sequence 22, App1
24	297.5	16.0	390	14	US-10-060-902-24 Sequence 24, App1
25	297.5	16.0	390	15	US-10-354-247-22 Sequence 22, App1
26	297.5	16.0	390	15	US-10-354-247-24 Sequence 24, App1
27	294.5	15.8	433	14	US-10-060-902-20 Sequence 20, App1
28	294.5	15.8	433	15	US-10-354-247-20 Sequence 20, App1
29	294	15.8	388	14	US-10-060-902-16 Sequence 16, App1
30	294	15.8	388	15	US-10-354-247-16 Sequence 16, App1
31	294	15.8	407	14	US-10-060-902-18 Sequence 18, App1
32	294	15.8	407	15	US-10-354-247-18 Sequence 18, App1
33	293.5	15.7	365	14	US-10-060-902-32 Sequence 32, App1
34	293.5	15.7	365	15	US-10-354-247-32 Sequence 32, App1
35	292.5	15.7	369	16	US-10-408-765A-176 Sequence 176, App
36	292.5	15.7	407	14	US-10-198-070-104 Sequence 104, App
37	291.5	15.6	374	14	US-10-060-902-30 Sequence 30, App1
38	291.5	15.6	374	15	US-10-354-247-30 Sequence 30, App1
39	291.5	15.6	393	14	US-10-060-902-36 Sequence 36, App1
40	291.5	15.6	393	15	US-10-354-247-36 Sequence 36, App1
41	291.5	15.6	402	14	US-10-225-567A-294 Sequence 294, App
42	291.5	15.6	402	14	US-10-060-902-34 Sequence 34, App1
43	291.5	15.6	402	15	US-10-354-247-34 Sequence 34, App1
44	291.5	15.6	425	14	US-10-060-902-26 Sequence 26, App1
45	291.5	15.6	425	15	US-10-354-247-26 Sequence 26, App1

ALIGNMENTS

US-10-225-567A-287	RESULT 1	US-10-320-351-3
Sequence 287, Application US/10225567A		
Publication No. US20030113798A1		
GENERAL INFORMATION:		
APPLICANT: Lifespan Biosciences		
APPLICANT: Brown, Joseph P.		
APPLICANT: Burner, Glenna C.		
APPLICANT: Roush, Christine L.		
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS		
FILE REFERENCE: 1920-4-4		
CURRENT APPLICATION NUMBER: US/10/225,567A		
CURRENT FILING DATE: 2001-12-19		
PRIOR APPLICATION NUMBER: 60/257,144		
PRIOR FILING DATE: 2000-12-19		
NUMBER OF SEQ ID NOS: 2292		
SOFTWARE: Patent version 3.1		
SEQ ID NO 287		
LENGTH: 359		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-10-225-567A-287		
Query Match	100.0%	Score 1864; DB 14; Length 359;
Best Local Similarity	100.0%	Pred. No. 2.5e-173; Indels 0; Gaps 0;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1	MMSPFYRCNTTSVEKNSAVMGVLFSTGLGNLALGLARSGLGWCSRRLRLPSV 60
DB	1	MMSPFYRCNTTSVEKNSAVMGVLFSTGLGNLALGLARSGLGWCSRRLRLPSV 60
OY	61	FYMLVGLVTVTLGLKCLSPVLAAYKQNRSLRVLAAPLDNSLCAFAFPMSFGLSST 120
DB	61	FYMLVGLVTVTLGLKCLSPVLAAYKQNRSLRVLAAPLDNSLCAFAFPMSFGLSST 120
OY	121	LQLLMALEKWLSTGHFFYRRHITLRLGALVAVPVVASFSLAFCAFPFGFGKFGVYCPG 180

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Db      121 LQLLAMLECMLESLGHPFFRRHTTLTLGALVAPVSAFSLAFALPFGMGFKVQCPG 180
Qy      181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAATVLCNIGAMRLYAMHRLQHRPSC 240
Db      181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAATVLCNIGAMRLYAMHRLQHRPSC 240
Qy      241 RDCAEPRADREASPOPLEEDHLLLLALMTVLFMTCSLPVIYRAYGAFDVEKRTS 300
Db      241 RDCAEPRADREASPOPLEEDHLLLLALMTVLFMTCSLPVIYRAYGAFDVEKRTS 300
Qy      301 EEAEDLALRFLSVISIVDPWIFIFRSPVRFIFRHKIFIRPLRYRSCNSTMSSL 359
Db      301 EEAEDLALRFLSVISIVDPWIFIFRSPVRFIFRHKIFIRPLRYRSCNSTMSSL 359

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RESULT 2
US-10-276-774-2370
; Sequence 2370, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyaeq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2370
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2370

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Query Match      100.0%; Score 1864; DB 15; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.8e-173;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKSPFYRCQNTTSYKGNASAVMGVLFSTGLGNLALGLARSGLCMSRRPLRPSPV 60
Db      41 MKSPFYRCQNTTSYKGNASAVMGVLFSTGLGNLALGLARSGLCMSRRPLRPSPV 100
Qy      61 FYMLVCGIYVTDLLGKCLSPVLAAYANQNSLRVLAPALDNLCOAFAPFMSFGLSST 120
Db      101 FYMLVCGIYVTDLLGKCLSPVLAAYANQNSLRVLAPALDNLCOAFAPFMSFGLSST 160
Qy      121 LQLLAMLECMLESLGHPFFRRHTTLTLGALVAPVSAFSLAFALPFGMGFKVQCPG 180
Db      161 LQLLAMLECMLESLGHPFFRRHTTLTLGALVAPVSAFSLAFALPFGMGFKVQCPG 220
Qy      181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAATVLCNIGAMRLYAMHRLQHRPSC 240
Db      221 TWCFIQWHEGSGSVGYSLVSSLMALLVLAATVLCNIGAMRLYAMHRLQHRPSC 280
Qy      241 RDCAEPRADREASPOPLEEDHLLLLALMTVLFMTCSLPVIYRAYGAFDVEKRTS 300
Db      281 RDCAEPRADREASPOPLEEDHLLLLALMTVLFMTCSLPVIYRAYGAFDVEKRTS 340
Qy      301 EEAEDLALRFLSVISIVDPWIFIFRSPVRFIFRHKIFIRPLRYRSCNSTMSSL 359
Db      341 EEAEDLALRFLSVISIVDPWIFIFRSPVRFIFRHKIFIRPLRYRSCNSTMSSL 399

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RESULT 3
US-10-225-567A-291
; Sequence 291, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:

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; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-8
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 291
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-291

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Query Match      37.0%; Score 689; DB 14; Length 358;
Best Local Similarity 43.7%; Pred. No. 1.3e-58;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

Qy      8 CQNTTSYKGNASAVMGVLFSTGLGNLALGLARSGLC--WCSRRPLRPSPVFMV 65
Db      13 CQNTTSYKGNASAVMGVLFSTGLGNLALGLARSGLC--WCSRRPLRPSPVFMV 71
Qy      66 CGLTVTDLLGKCLSPVLAAYANQNSLRVLAPALDNLCOAFAPFMSFGLSSTIQLLA 125
Db      72 TELVFDLQTCILSPVLAAYANQNSLRVLAPALDNLCOAFAPFMSFGLSSTIQLLA 129
Qy      126 MALECWLSLGHPPFRRHTTLTLGALVAPVSAFSLAFALPFGMGFKVQCPGTCF 185
Db      130 MALECWLSLGHPPFRRHTTLTLGALVAPVSAFSLAFALPFGMGFKVQCPGTCF 189
Qy      186 QWHEGSGSVGYSLVSSLMALLVLAATVLCNIGAMRLYAMHRLQHRPSC 245
Db      190 R--HGR-----YALDLYATLLLVSVLACNFSVILNIRHRSRR--SRGSGSLGS 240
Qy      246 ----PRADREASPOPLEEDHLLLLALMTVLFMTCSLPVIYRAYGAFDVEKRTS 301
Db      241 GRGPGARRGERVSAEFTDHLILALMTITRACVSLPTIRAY-----METSS 291
Qy      302 EAE--DIRALRFLSVISIVDPWIFIFRSPVRFIFRHKIFIR--PLRYRSCNSTM 357
Db      292 RKEMDQLRFLSVISIVDPWIFIFRSPVRFIFRHKIFIR--PLRYRSCNSTM 350

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RESULT 4
US-10-352-684A-36
; Sequence 36, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; FILE REFERENCE: MP102-019P1RNONNIM
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/10/352,684A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26

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Query Match	37.0%;	Score 689;	DB 15;	Length 358;
Best Local Similarity	43.7%;	Pred. No. 1.3e-58;		
Matches 157;	Conservative 54;	Mismatches 118;	Indels 30;	Gaps 10;

RESULT 5
US-10-366-288-36
Sequence 36, Application US/10366288
Publication No. US20030216288A1
GENERAL INFORMATION:
APPLICANT: Powell, Douglas
APPLICANT: Welch, Nadine S.
TITLE OR INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OR INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,
TITLE OR INVENTION: 34021, 1710, 1683, 1552, 1687, 12825, 9952, 5816,
TITLE OR INVENTION: 10002, 1671, 1371, 14324, 126, 270, 312, 167, 326, 18926
TITLE OR INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
FILE REFERENCE: MP102-025P:RNOMNT
CURRENT APPLICATION NUMBER: US/10/366, 288
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 60/357, 391
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380, 249
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/391, 306
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/406, 297
PRIOR FILING DATE: 2002-08-27

Query Match	37.0%;	Score 689;	DB 15;	Length 358;
Best Local Similarity	43.7%;	Pred. No. 1.3e-56;		
Matches 157;	Conservative 54;	Mismatches 118;	Indels 30;	Gaps 10

RESULT 6
US-10-755-889-92

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? APPLICANT: Bristol-Myers Squibb Company
? TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF- $\kappa$ B
? TITLE OF INVENTION: PATHWAY
? FILE REFERENCE: D0284 NP
? CURRENT APPLICATION NUMBER: US/10/755,889
? CURRENT FILING DATE: 2004-01-13
? PRIOR APPLICATION NUMBER: U.S. 60/440,068
? PRIOR FILING DATE: 2003-01-14
? PRIOR APPLICATION NUMBER: U.S. 60/469,757
? PRIOR FILING DATE: 2003-05-12
? NUMBER OF SEQ ID NOS: 823
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 92
? LENGTH: 358
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-755-889-92

Query Match      37.0%; Score 689; DB 16; Length 358;
Best Local Similarity 43.7%; Pred. No. 1,3e-58;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY      8  CQNTTSVEKNSANMGCVLPFTGLLGNLLAAGLARSLG--WGRRRPLRLPLPSVFYMLV 65
      13  CRRQWLPPEESPAPSISSWFSAGVLGNLIALALLARRRGVGVGSAGRRSSL-SLEFHYLV 71

```



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      | | | | | : | : | : | : | : | :
269 S S E M G D L A F R Y A F N P I L D P W V F I L R K A V Q 301
Db

```

RESULT 12
US-10-108-260A-3907
; Sequence 3907, Application US/10108260A
; Publication No. US20040005560A1

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1  APPLICANT: HELIX RESEARCH INSTITUTE
2  TITLE OF INVENTION: No. US0040005560A1el full length cdnna
3  FILE REFERENCE: H1-A0106
4  CURRENT APPLICATION NUMBER: US/10/108,260A
5  CURRENT FILING DATE: 2002-03-27
6  NUMBER OF SEQ ID NOS: 5458
7  SOFTWARE: PatentIn Ver. 2.1

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US-10-108-260A-3907

Query Match	27.8%	Score 518.5	DB 15	Length 289
Best Local Similarity	43.3%	Pred No. 4.6e-42		
Matches 122	Conservative 39	Mismatches 82	Indels 39	Gaps 8

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Oy      8  CQNTTSVEKGNASVMGGVLFSTGLLGNTLALGLLARSGLGCSSRRPLRLPSPVFMVLVCG  67
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      5  CRNLTVRGSGVCPATSTLTFVAGVWNGIALGLIS-----ARRPAR--PSAFVAVLVTG  55

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```

Oy      68  LTVDDLGGKCLISPVLLAAVQNRSLRVLA---PALNSLCCQAFPFMFSPGISTLQL 124
      |||||  |||||  :|||  |||||  :|||  :|||  :|||  :|||  :|||  :|||
Db      56  LAATULLGSTLSPAVFVAYARNSSLEGLARGSPA----LCDAFAPAMTFGLASMLIF 111

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```
OY      125 AMALECWLSLGHPPFFRRRHITLRGLVA PVVSAFSLAFCALPFMGEGKGVQCPGTGCF 18
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      112 AMAVERCLATSHRYLAQLDGBRCARLATPAIYAFVLGCALPLLGLQHQQCPGSGWCF 17
```

```

Oy      185  IQM--VHEEGLSVLGYSLVYSSLMALLVLAIVLCNLCAGMRNIYAMHRRLQRPSCRSD 242
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      172  LRMRWAPGGA---AFSLAIVAGLVALLVAALFLCNGSVTLISLCRMVQDQKRIQGS---- 223

```

```

Oy      243 CAEPRADGREASPOPL--EELDHLILLALMTVLFTMCSLPV 281
          | : | : | | | | | | | : | | | |
Db      224 -----LGRPRTEGEVDHLILLALMTVMVAVCSLP 255

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RESULT 13
US-10-225-567A-296

? Publication No. US20030113798A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Lifespan Biosciences
 ? APPLICANT: Brown, Joseph P.
 ? APPLICANT: Burner, Glenna C.
 ? APPLICANT: Roush, Christine L.
 ? TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ? FILING DATE: 1997-04-04

US-10-225-567A-296

Query Match	23.8%	Score 443	DB 14	Length 488
Best Local Similarity	31.9%	Pred. No. 2.1e-34		
Matches 126	Conservative 63	Mismatches 149	Indels 58	Gaps 13

```

Qy      1 MKSPYRCQNTTSVEKNSAV-MGVLFSTGLLGNLLAGLLASGIGWCSRRPLRLPLPS 53
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      1 MSTPGVNSSASLSPDRLNSPTTIPAWMFIFGVGNLVAIVLWCK-----SRKEQK-ET 52

```

```
Qy      60 VFVNLVCGLTVTDLIGCKLISPVLAAYAQNRSLRVLPALDNLSCQAFAFNSFFGLSS 119
        ||||| | | | | : ||| : | : : ||| | | | |
Db      53 TPTVLVCGLAVTDLGTLVSPVLIATYMKQ-----WPG-GQLPCXSTFIILFFSLSG 106
```

Qy 120 TLQLLMALECWLSLGHPFFYRHHITLRGLAVAPVSAFSLAFCALPFMGFKFYQYCP 179
: : : : : : : : : : : : : : : :
Db 107 LSIICAMSERYLAINHAVFYSHYVDKRLAGITLFAVYASNLFCAIPNMGICSSRIQYP 166

Qy 180 GTWCIQVMEHSGSLVGLSVLYSSLMALLVATVLCNLGLAMRNLYAMHRRLQRHPSC 239
 ||||| : || : : ||||| : ||| :
 Db 167 DTWCIDWT--TNVTAHAAYSVMYAGFSSFLIATVLCNVLCVCGALLRMHROEMRRTSLG 224

```

Qy      240 TRD-----CAEPRADGREALSQPL-----EELDHLLLLALMTVLPTMNC 277
          |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      225 TEQHHAAAAASVASRGHPAASPALPLSDFFRRRRSPFRIAGABIQWILLIATSLVVIC 284

```

QY 278 SLPLVYRAYYGAFKQVKEKKEKRTSEAE-----DLRLRLFLSTISIVDWPIFLFRSPYER 3322

DB 285 SIPLVVRVF-----VNQLYQPSLEEVSKNPDQLAIRIASVNPILDPWIYILLRKTIVLS 338

```

QY      333  IFHKT---FIR---PLRYRS--RCSNSTNMWSSL 355
          ||      ||      ||      ||      ||      ||
DB      339  KAIEXIKCLFGRIGSRNRERQCHCSDSQRTSSAM 373

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RESULT 14
US-10-320-351-3

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? PUBLICATION NO. US2003013431A1
? GENERAL INFORMATION:
? APPLICANT: Carroll, Joseph M.
? APPLICANT: Healy, Aileen
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
? TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 252, 304, 1980, 14717, 9941
? TITLE OF INVENTION: 19310 AND 17832
? FILING DATE: 20030619

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ORGANISM: Homo sapiens
US-10-320-351-3

Query Match	23.8%	Score 443	DB 14	Length 488
Best Local Similarity	31.9%	Pred. No. 2.1e-34		
Matches 126; Conservative	62;	Mismatches 149;	Indels 58;	Gaps 13;

```
Qy      1 MKSPFYRCQNTTSVEKGN SAV-MGCVLFSTGLGNLALGILARSGLGCSSRPLRPLPSS
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      1 MSTPGNVSASASLPDRLNSPVTTPAVMFTFGVGNLVAIVLCK-----SRKEQK--ET
```

```
QY      60 VFVMLVCGLTWTDLGKCLLSPVILAAVAQNRLRVLAPALDNSLCOAFEFMSFFGLSS 113
        ||||| | | | | | : | | | : | | | | |
Db      53 TPTYLVCGLAVTDLGTLVSPVTIATYMKQG-----WPG-GQPLCESTFILLFFSLSG 106
```

```
QY      120 TLQLLMALECWLSLGHPFFXYRRHITRLGALVAPVVSASFSLAFCALPEFMGFKEVOYCP 176
          : |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      107 LSIICAMSVERYLLAINHAIFYSHYVDKRLAGLTLPATYASNVLCALPENMGSSSRLOYP 160
```

```

QY      180 GTWCFIQMWHEEGSLVGLSVLYSSIMALLVLTATVINC LGAMRNLYAMHRRPLQRHPSC 233
          |||||      : ||| : : ||||| : ||| :
Db      167 DTWCFFIDWT--TNTVTAHAAYSIMYAGSSFLLIATVINCVLVCGALLRMHRRQFMRITSLG 222

```



```

OY      240 RD-----CAEBRACRGREASPOPL-----BEDJHLLLLMTATVFTMC 277
          |      |      |      |      |      |      |      |      |
Db      225 TEOHHAAAASVASKRHPAASPALPLSDPFRRRRRSRRRAGATIQWILATISLVLIC 284
          |      |      |      |      |      |      |      |      |
OY      278 SLPLVIRAYVYGAFKDKVKERNRTSEAE-----DLRALRFLSVISYDPMFIIFRSPPVR 332
          |:::|      |      |      |      |      |      |      |
Db      265 SIPLVVRVF-----VNOIYQPSLEEVSKNPDLOAIRASVNPILDPMWITILKRTVLVS 358
          |      |      |      |      |      |      |      |      |
OY      333 IFPHKI---FIR---PLRYRS--RCGNSNTMESSL 359
          ||      |      |      |      |      |      |      |
Db      339 KAIETIKCLFCRIIGSRRRERSQHCHDSQRTSSAM 373

```

```

RESULT 15
US-10-295-027-1326
; Sequence 1326, Application US/10295027
; Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT FILING DATE: 2002-11-13
PRIORITY FILING DATE: 2002-11-13
PRIORITY APPLICATION NUMBER: US 09/663,733
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 60/350,666
PRIORITY FILING DATE: 2001-11-13
PRIORITY APPLICATION NUMBER: US 60/335,394
PRIORITY FILING DATE: 2001-11-15
PRIORITY APPLICATION NUMBER: US 60/332,464
PRIORITY FILING DATE: 2001-11-21
PRIORITY APPLICATION NUMBER: US 60/334,393
PRIORITY FILING DATE: 2001-11-29
PRIORITY APPLICATION NUMBER: US 60/340,376
PRIORITY FILING DATE: 2001-12-14
PRIORITY APPLICATION NUMBER: US 60/347,211
PRIORITY FILING DATE: 2002-01-08
PRIORITY APPLICATION NUMBER: US 60/347,349
PRIORITY FILING DATE: 2002-01-10
PRIORITY APPLICATION NUMBER: US 60/355,250
PRIORITY FILING DATE: 2002-02-08
PRIORITY APPLICATION NUMBER: US 60/356,714
PRIORITY FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1326
LENGTH: 488
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-1326

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Query Match	23.8%	Score	443	DB	15	Length	488
Best Local Similarity	31.9%	Pred. No.	2.1e-34				
Matches	126	Conservative	62	Mismatches	149	Indels	58
						Gaps	13

[illegible]

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Oy      120  TTGLLMALECMWLSGHPFFYRRHTTLTGALVAVPVSAFSLACALPFMGFGFVQCP      179
      107  LSTICAMSVERTIALNHAFYSHYVDKRLAGLTLEFAYASVULFCALEPNNGLSSRIQYP      166
Oy      180  GTWCPIQWHEBGSLGYSVLVSSMLLVLTATVLCIGAMENLYAMERRLORHPSC      239
      167  DTWCPIQWHEBGSLGYSVLVSSMLLVLTATVLCIGAMENLYAMERRLORHPSC      224
      167  DTWCPIQWHEBGSLGYSVLVSSMLLVLTATVLCIGAMENLYAMERRLORHPSC      224
Oy      240  TRD-----CAEPADGREGASPOPL-----EEGLDHLILLALMTVLPFTMC      277
      225  TEGHMAAAASVASKGHAPASPALRLSDPPRRRSFRRIAGAEQWIVILLIANSVLVLC      284
Oy      278  SLEVIYRAYGAFKOVKEKRTSEBAE-----DLPALEFVSISVDPWFIIIFRSEVFR      332
      285  SLEVIYRAYGAFKOVKEKRTSEBAE-----DLPALEFVSISVDPWFIIIFRSEVFR      338
Db      285  SLEVIYRAYGAFKOVKEKRTSEBAE-----DLPALEFVSISVDPWFIIIFRSEVFR      338
Oy      333  IFPHKI---FIR---PLRYRS--RCSTNGTNNESG      359
      339  KALEKIKLCPFRIGSRREGRSGHSDQORRISAM      373

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Job time : 187.351 secs

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